

2004-10-32 16:10

US-10-015-480a-180.rni

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame_plus_p2n model

April 9, 2004, 10:40:36 ; Search time 86 Seconds
(without alignments)
1432.548 Million cell updates/sec

US-10-015-480a-180

1189
1 MPKTMHFLFRFVFFYVWGL.....HDGDFISPKENVVQHDEL 222

BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 1365418

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

FMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

OP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	971	4	US-09-205-258-33		Sequence 33, Appl
98.9	968	4	US-09-205-258-222		Sequence 222, App
24.9	575	4	US-09-833-381-1564		Sequence 1564, Ap
20.9	570	1	US-07-822-9668-1		Sequence 1, Appli
20.5	562	5	PCT-US92-03993-6		Sequence 6, Appli
20.5	2610	2	US-08-989-386-2		Sequence 2, Appli
16.9	964	4	US-09-023-655-1081		Sequence 1081, Ap
15.7	2157	1	US-08-336-618-25		Sequence 25, Appl
15.6	450	4	US-09-621-976-2544		Sequence 2544, Ap
15.6	675	1	US-08-707-793A-3		Sequence 3, Appli
15.0	571	2	US-08-803-899-1		Sequence 1, Appli

13	176	14.8	2291	4	US-09-220-132-114	Sequence
14	175	14.7	411	4	US-09-481-620A-84	Sequence
15	174.5	14.7	327	3	US-09-012-515A-34	Sequence
16	174.5	14.7	327	3	US-08-360-144A-34	Sequence
17	174.5	14.7	327	4	US-09-012-504A-34	Sequence
18	174.5	14.7	327	4	US-09-012-399A-34	Sequence
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22	174.5	14.7	348	4	US-09-012-399A-5	Sequence
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24	174.5	14.7	690	4	US-09-481-620A-110	Sequence
25	174.5	14.7	1137	1	US-08-707-793A-1	Sequence
26	174.5	14.7	1137	1	US-08-707-792A-1	Sequence
27	174.5	14.7	1155	1	US-08-707-792A-2	Sequence
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29	173	14.6	2246	4	US-09-566-921-48	Sequence
30	172	14.5	443	4	US-09-833-381-1562	Sequence
31	167	14.0	2255	2	US-08-741-134-1	Sequence
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33	166.5	14.0	405	4	US-09-621-976-15602	Sequence
34	166	14.0	357	4	US-09-328-352-1668	Sequence
35	165	13.9	459	4	US-09-833-381-693	Sequence
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44	136.5	11.5	765	4	US-09-489-039A-3743	Sequence
45	136	11.4	1401	4	US-09-252-991A-4911	Sequence

ALIGNMENTS

RESULT 1

US-09-205-258-33

; Sequence 33, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: PZ007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; EARLIER FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

ICATION NUMBER: 60/048,882
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,899
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,893
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,900
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ICATION NUMBER: 60/048,901
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NG DATE: 1997-06-06
ICATION NUMBER: 60/048,877
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,878
NG DATE: 1997-06-06
ICATION NUMBER: 60/070,923
NG DATE: 1997-12-18
ICATION NUMBER: 60/092,921
NG DATE: 1998-07-15
ICATION NUMBER: 60/094,657
NG DATE: 1998-07-30
tentIn Ver. 2.0

lomo sapiens

ITE
(957)
INATION: n equals a,t,g, or c
ITE
(964)
INATION: n equals a,t,g, or c
33

35: 4.44e-143 Length:
1189.00 Matches:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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Qy 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG:
Db 139 TTTACTGCTCAGAGACAAAAGAAAGAGAGAGACCCGAGAGAGTGAATAAG:
Qy 41 HisArgProGluLysSerLysThrSerLysLysGlyAspLeuLeuAsnA:
Db 199 CATGCTCCAGAAAACCTGCTCTAAAGACAAAGCAAGAGAGAGACCTTAAATG:
Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA:
Db 259 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACGCGGACACAA:
Qy 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspI:
Db 319 CACCCCAATGGTTTGTCTTGGTGTGGCAAGTCATATAAAGGCGCTAGACA:
Qy 101 ThrAspMetCysProGlyGluLysArgLysValValleProProSerPheA:
Db 379 ACAGATATGTCCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTG:
Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG:
Db 439 AAGGAAGCTATGCAAGAGCAAGATTCACCGGATGCTACATTGATTTTG:
Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA:
Db 499 CTTTATGCTGTGACCAAGGACACCGGAGCATTGAGACATTTAAACAAATAG:
Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGluArgGluP:
Db 559 AATGACAGGCGCTCTCTAAAGCGGAGATAAACCTCTACTTGAAGGGGAAT:
Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP:
Db 619 GATGAGAAGCCACGTGACAAAGTCATATCAGATGCACTTTTAGAGATATT:
Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG:
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Qy 221 GluLeu 222
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; Sequence 222, Application US/09205258
; Patent No. 525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06

ID NOS: 1227

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; SEQ ID NO 222
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (954)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (961)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-222

Alignment Scores:
Pred. No.: 2,06e-141
Score: 1176.00
Percent Similarity: 99.55%
Best Local Similarity: 99.55%
Query Match: 98.91%
DB: 4

US-10-015-480A-180 (1-222) x US-09-205-258-222 (1-968)

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QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeu-AsnA
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QY 60 rAspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
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QY 80 yHisProLysTrrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
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QY 100 tThrAspMetCysProGlyGluLysArgLysValIleProProSerPheA
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QY 120 YLysGluGlyTyrAlaGluGlyLysileProProAspAlaThrLeuIlePheG
Db 434 AAAGGAGGCTATGCAAGAGGCAAGATTCACCGATGCTCATGATATTTTTG

QY 140 uLeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
Db 494 ACTTTATGCTGTGACCAAGGACCACGAGCATTCAGACATTTAAACCAATAGJ

QY 160 pAsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
Db 554 CAATGACAGCGAGCTCTCTTAAAGCCGAGATAAACCTCTACTTTGCAAGGGAAT

QY 180 sAspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
Db 614 AGATGAGAGCCACGTGCAAGTCATATCAGATGCAGTTTGTAGAGATATTT

QY 200 sAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
Db 674 GAATCAGCATGATGGTGTGGCTTCATTTCTCCCAAGGAATACATGATATACCA


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; Application PC/TUS9203993
; MATION:
; Harding, Matthew W.
; INVENTION: REKEP: A NOVEL PROLYL ISOMERASE AND
; INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
; SEQUENCES: 10
; NCE ADDRESS:
; : Hamilton, Brook, Smith & Reynolds, P.C.
; : Two Militia Drive
; : xington
; : USA
; 73
; ADABLE FORM:
; PE: Floppy disk
; IBM PC compatible
; SYSTEM: PC-DOS/MS-DOS
; PatentIn Release #1.0, Version #1.25
; LICATION DATA:
; ON NUMBER: PCT/US92/03993
; TE: 19920507
; ATION:
; CATION DATA:
; ON NUMBER: US 07/697,113
; TE: 08-MAY-1991
; ENT INFORMATION:
; anahan, Patricia
; ION NUMBER: 32,227
; /DOCKET NUMBER: VP191-05A PCT
; CATION INFORMATION:
; : (617) 861-6240
; (617) 861-9540
; OR SEQ ID NO: 6:
; ARACTERISTICS:
; 562 base pairs
; CLEIC ACID
; ESS: double
; linear
; PE: DNA (genomic)
;
;
; 4.52e-22 Length: 562
; 244.00 Matches: 55
; ty: 63.25% Conservative: 19
; arity: 47.01% Mismatches: 19
; 20.52% Indels: 4
; 5 Gaps: 3
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; rLysLysGlyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAlaLysAspGlySer 69
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; sPheTyrCysSerArgThrGluAsnGluGlyHisProLysTrpPheValLeuGlyVal 89
; GTTTGACACAGCGCTGCCCGCAGAACCCAG-----CCCTTTGTCTTCTCCCTTTGGCACA 276
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Qy 130 ProProAspAlaThrLeuIlePheGluIleGluLeuTyrAlaValThrLys 1
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US-08-989-386-2
; Sequence 2, Application US/08989386
; Patent No. 5989860
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT01
; CLONE: 2255114
; US-08-989-386-2
Alignment Scores:
Pred. No.: 5.22e-21 Length: 2610
Score: 243.50 Matches: 65
Percent Similarity: 52.61% Conservative: 46
Best Local Similarity: 30.81% Mismatches: 69
Query Match: 20.48% Indels: 31
DB: 2 Gaps: 10
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Qy 35 ValLysIleGluValLeuHisArgPro---GluAsnCysSerLysThrSerLys
Db 1186 GTGGAATCAGGACACTGTCCCGCCCATCTCAGACCTGCAATGAGACCCAG
Qy 54 AspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAlaLysAspGlySerLysPhe
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rProSerPheAlaTyrgLysGluGlyTyraLaGluGlyLysIleProProAspAla 133
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brLeuIlePheGluLeuTyraLaValThrLysGly----- 147
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
TGCTGCTGTTGAGTGGAGCTGGTGTCCGGGAGATGGGCTGCCACAGGCTACCTG 1530
-----ProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTGTGTGGCACAAGGACCTCTGCCAAGCTG-----TTTGAAGCATGGACCTCAAC 1584
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
sAspArgGlnLeuSerLysAlaGluIleAsnLeuTyraLeuGlnArgGluPheGluLys 180
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spGluLysProArgAspLysSerTyrgLysPhe-----AlaValLeuGluAspIlePhe 139
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ysLysAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyraAsnValTyrgL 218
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-----HisAspGluLeu 222
ATGAGACGAGGAGCGGGTCCACGAGGAGCTC 1794

```

081

Application US/09023655
07879

RMATION:

Cocks, Benjamin G.

Susan G. Stuart

Jeffrey J. Seilhamer

VENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

SEQUENCES: EXPRESSION

SEQUENCES: 1508

3: INCYTE PHARMACEUTICALS, INC.

3174 PORTER DRIVE

ALO ALTO

CALIFORNIA

USA

304

ZADABLE FORM:

IEM PC compatible

3: SYSTEM: PC-DOS/MS-DOS

PLICATION DATA: Word Perfect 6.1 for Windows/MS-DOS 6.2

ION NUMBER: US/09/023,655

ATE: HEREWITH

CATION:

ION DATA:

ION NUMBER:

ATE:

CATION:

SENT INFORMATION:

aller, Karen J.

ION NUMBER: 37,071

3/DOCKET NUMBER: PA-0001 US

ICATION INFORMATION:

3: (650) 855-0555

(650) 845-4166

; INFORMATION FOR SEQ ID NO: 1081:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 964 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g182625

US-09-023-655-1081

Alignment Scores:

Pred. No.: 3,91e-16

Score: 200.50

Percent Similarity: 45.10%

Best Local Similarity: 29.41%

Query Match: 16.86%

Indels: 61

Gaps: 7

US-10-015-480A-180 (1-222) x US-09-023-655-1081 (1-964)

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Db 219 CTTTITTTGAAACTAAGCGTTTAAAGGCTACTGAAAGTATAAGTAAAGCTGTCTGA

QY 40 LeuHis-----ArgProGluAsnCys-----

Db 279 AAAAATGTGAAGCTTAATGAAGATAAACCCAAAGAAACCAAGCTCTGAAGAGAC

QY 47 -----SerLysThrSe

Db 339 GAGGGTCCACCAAAATATATACTTTCTGTTCTGAAAAGGAGATATAAACCAA

QY 51 LysLysGlyAspLeuLeuAsnAlaHisTyraAspGlyTyraLeuAlaLysAspGl

Db 399 AAAAGGAGAGATGTGTTCACCTGCTGTATACAGGAACACTA---CAAGATGG

QY 71 Phe-----TyrCysSerArgThrGlnAsnGluGlyHisProLy

Db 456 TTTGACTACTAATATTCAAACAAGTCCAAAGAGAGAGAAATGCCAAGCTTT

QY 86 ValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMetThrAspMe

Db 516 AAGGTCGGAGTAGGCAAGTTATCAGAGATGGGATGGAAGCTCTCTTGACTAT

QY 106 GlyGluLysArgLysValValIleProProSerPheAlaTyrgLysGluGl

Db 576 GGAGAAAGGCTCGACTGGAGATTGAACCAAGATGGGCTTACGGAAGAAAGG

QY 126 GluGlyLysIleProProAspAlaThrLeuIlePheGluIleGluLeuTyraI

Db 636 GATGCCAAATTCACCAATGCAAACTCCTTTTGAAGTGAATTA-----

QY 146 LysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAspAr

Db 684 -----GTGGATATTGATTGAATAG

QY 166 SerLysAlaGluIleAsnLeuTyraLeuGlnArgGluPheGluLysAspGluLy

Db 711 TTCASCTCT-----AAGGATATTAG

QY 186 AspLysSerTyra 189

Db 738 GATAAAACTGG 749

RESULT 8

US-08-336-618-25

; Sequence 25, Application US/08336618

; Patent No. 5763590

; GENERAL INFORMATION:

; APPLICANT: Peattie, Debra A.

; APPLICANT: Harding, Matthew W.

; APPLICANT: Livingston, David J.

ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,899
FILING DATE: 02/21/1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/012,054
FILING DATE: 02/22/1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: STEFF, ERIC K

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4240001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 base pairs

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..324
803-899-1

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No.:	1.38e-13	Length:	571
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nt Similarity:	57.84%	Conservative:	39
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Match:	14.97%	Indels:	4
	2	Gaps:	3

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 28 CCTGGTGGTGGCAGCACCTATCCAGAATGSCCAAAAGTCACGCTCCACTA:
 63 ThrLeuAlaValAsnGlySerIysPheThrCysSerAspSerGlyCysSerGlyGly:

88 ACCCG---GACGATGGCACAAGTTTCGATTCGTGCGCGACCGCAACAAG---
83 LysTrpPheValIeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet
139 TTCAGTTCCACATCGGCAAGGGCGAGGTCATCCGTTCGGATCGAGGGATTC

[illegible]

259 GGCCAC---CCGGGTCATTCCGGCCAACTCCACCTCACCTTGCACGTCGAC
143 AlaVal 144
316 AAGGTC 321

-220-132-114
Sequence 114, Application US/09220132
Patent No. 6506607

GENERAL INFORMATION:
 APPLICANT: Shviken
 Andrew W

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ENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
ENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
CE: 07334-074301
ICATION NUMBER: US/09/220,132
NG DATE: 1998-12-23
ATION NUMBER: US 60/079,303
DATE: 1998-03-25
ATION NUMBER: US 60/068,821
DATE: 1997-12-24
Q ID NOS: 191
astSEQ for Windows Version 4.0

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1

omo sapiens
114

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larity: 30.51% Mismatches: 56
 Indels: 14.80%
 Gaps: 5

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ATGTCATTACAAAGGAATAATGTCA--AATGGAAAGATTGATCCAGTCATGAT 193

lnAsnGluGlyHisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeu 96
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ACTATGGGTGGCTACCATTGAAGAAGGAGAGATGCCAATTACTGTGCAAACCGAA 307

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ATGCATATGGCTCGGTGGC---AGTCTCCCTAAAATTCCTCGAATGCAACTCTCTTT 364

heGluIleGluLeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGln 156
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TTGAGATTGAGTCTCCTT-----GATTCAAAGGA 394

leAspMetAspAsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArg 176
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
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luPheGluLysAspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAsp 196
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-----GGAGGC 418

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TTATCCGGAGACCAACCGAAGGAGGAGATATCAATCCAAACGA 469

84

Application US/09481620A
06379
MATION:
RIAD Gene Therapeutics, Inc.
ENTION: Rapamycin Based Regulation of Biological Events
CE: 345B PCT
ICATION NUMBER: US/09/481,620A
NG DATE: 2000-01-12

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; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 84
; TYPE: DNA
; LENGTH: 411
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCANTAB--AP--FKBP--
; NAME/KEY: misc_structure
; LOCATION: (1)..(411)
US-09-481-620A-84

Alignment Scores:
Pred. No.: 2,05e-13 Length: 411
Score: 175.00 Matches: 47
Percent Similarity: 51.08% Conservative: 24
Best Local Similarity: 33.81% Mismatches: 54
Query Match: 14.72% Indels: 14
DB: 4 Gaps: 5

US-10-015-480A-180 (1-222) x US-09-481-620A-84 (1-411)

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Db 46 -----GGGCGCCAGCGCGGCATGCGCGCAGGAGTGCAGGTGGAGACTAT
QY 43 ProGluAsnCySerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTy
Db 94 CCAGGAGAGCGGCGCACCTTCCCAAGCGCGGCAGACCTGCGTGGTGCACTA
QY 63 TyrLeuAlaLysAspGlySerLysPheThrCysSerArgThrGlnAsnGluGl
Db 154 ATGCTT--GAAGATGGAAGAAATTTGATTCCTCCGGGACAGAAACAAG--
QY 83 LysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMe
Db 205 TTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGGGAGAGGGGT
QY 103 MetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGl
Db 265 ATGAGTGTGGTCCAGAGAGCAAACTGACTATATCTCCAGATTATGCTATGG
QY 123 GlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGl
Db 325 GGGCAC--CCAGGCATCATCCACCATGTCCTCTGCTCTCGATGTGGA

RESULT 15
US-09-012-515A-34
; Sequence 34, Application US/09012515A
; Patent No. 6127521
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

April 9, 2004, 08:23:49 ; Search time 99 seconds
(without alignments)
5084.247 Million cell updates/sec

US-10-015-480A-179

907
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IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 1365418

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/ptcus_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
96.7	971	4	US-09-205-258-33	Sequence 33, Appl
95.0	968	4	US-09-205-258-222	Sequence 222, App
10.8	575	4	US-09-833-381-1564	Sequence 1564, Ap
7.3	5173	1	US-08-242-677-1	Sequence 1, Appli
7.2	10660	2	US-08-267-803B-8	Sequence 8, Appli
7.2	10660	3	US-09-041-886-16	Sequence 16, Appl
6.9	1129	4	US-09-227-357-40	Sequence 40, Appl
6.9	3994	4	US-09-738-946-7	Sequence 7, Appli
6.7	7724	4	US-08-486-049-1	Sequence 1, Appli
6.7	1776	3	US-08-655-352-10	Sequence 10, Appl
6.7	1776	4	US-09-258-016-10	Sequence 10, Appl
6.7	1776	4	US-09-257-825B-10	Sequence 10, Appl
6.7	964	4	US-09-023-655-1081	Sequence 1081, Ap
6.6	2205	3	US-08-888-077A-41	Sequence 41, Appl
6.6	2058	2	US-08-749-391-1	Sequence 1, Appli
6.6	2058	3	US-09-390-200-1	Sequence 1, Appli
6.6	3200	1	US-08-444-405-1	Sequence 1, Appli
6.6	3200	1	US-08-384-850-1	Sequence 1, Appli
6.6	972	4	US-09-549-831-5	Sequence 5, Appli
6.6	2381	1	US-08-021-608D-9	Sequence 9, Appli
6.6	2381	1	US-08-726-160-9	Sequence 9, Appli
6.6	2381	5	PCT-US94-01782-9	Sequence 9, Appli
6.6	2384	1	US-08-021-608D-1	Sequence 1, Appli
6.6	2384	1	US-08-726-160-1	Sequence 1, Appli
6.6	2384	5	PCT-US94-01782-1	Sequence 1, Appli
6.5	1357	4	US-09-461-325-55	Sequence 55, Appl
6.5	1357	4	US-10-012-542-55	Sequence 55, Appl

28	58.8	6.5	2852	3	US-09-027-137-2	Sequenc
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30	58.6	6.5	1618	4	US-09-800-729-29	Sequenc
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45	58	6.4	2438	4	US-09-393-634-4	Sequenc

ALIGNMENTS

RESULT 1

US-09-205-258-33
; Sequence 33, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
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; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
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; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

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 IG DATE: 1997-12-18
 ICATION NUMBER: 60/092,921
 IG DATE: 1998-07-15
 ICATION NUMBER: 60/094,657
 IG DATE: 1998-07-30
 ID NOS: 1227
 entIn Ver. 2.0

mo sapiens

TE

; LOCATION: (241)
 ; OTHER INFORMATION: n equals a,t,g, or c
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 ; NAME/KEY: SITE
 ; LOCATION: (954)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (961)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-205-258-222

Query Match 95.0%; Score 861.6; DB 4; Length 968;
 Best Local Similarity 99.1%; Pred. No. 6.8e-182;
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QY	780	TTTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTTGGTAT
Db	832	TTTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTTGGTAT
QY	840	GTGAGGCTGTTTTCGCAAACTTAAAAAAGGAAAAAAGGAAAAA 879

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 TGAGCGTCTTTTGCACAACTTAAAAAATTTAAAAAAA 931

564
 Application US/09833381

72186

MATION:

obison, Keith E.

ENTION: No. 6672186el Nucleic Acid and Protein Homologs

CE: 5800-119

ICATION NUMBER: US/09/833,381

NG DATE: 2001-04-11

ATION NUMBER: 09/516,448

DATE: 2000-02-29

Q ID NOS: 2050

stSEQ for Windows Version 3.0

4

omc sapiens

564

10.8%; Score 97.6; DB 4; Length 575;

ilarity 59.3%; Pred. No. 6.8e-13;

Conservative 0; Mismatches 114; Indels 0; Gaps 0;

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3ACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTACTG 240

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3ATTTGATGTGGTCCACTATGAGGCTACTTAGAAAAGCAGGCTCTTTTCACTC 382

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ACCGGACAAAATGAGGCGCACCCCAATGGTTTGTCTTGGTGTGGGCAAGTCAT 300

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ACTCAAAACATAACAATGGTCAGGCCATTGGTTTACCTGGGCATCTCGAGGCTCT 442

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MAAGCTAGACATTGCTATGACATATGTCCTCGGAGAAAGCGAAAGTATTAT 360

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MAAGTTGGGACGAGGCTTGAAGGAATGTGTAGGAGAGAGAAAGTCATCAT 502

CCCCCTCATTTGCATACGGAAGGAGGCTATGCAGAA 400

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CTCCTGCTCTGGCTATGGAAGGAGGAAAGGTAAA 542

pplication US/08242677

77143

INATION:

Gaynor, Richard B

Wu, Foon W.

VENTION: Cellular Nucleic Acid Binding Protein

VENTION: and Uses thereof in regulating Gene Expression and in the

VENTION: Treatment of AIDS

SEQUENCES: 9

ANCE ADDRESS:

S: Arnold, White & Durkee

P.O. Box 4433

ouston

TX

USA

210

SADABLE FORM:

YPE: Floppy disk

: IBM PC compatible

3 SYSTEM: PC-DOS/MS-DOS

: PatentIn Release #1.0, Version #1.25

PLICATION DATA:

APPLICATION NUMBER: US/08/242,677

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mayfield, Denise L.

REGISTRATION NUMBER: 33,732

REFERENCE/DOCKET NUMBER: UTSD:401

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-787-1400

TELEFAX: 713-789-2679

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5173 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..4863

US-08-242-677-1

Query Match

Best Local Similarity 7.3%; Score 65.8; DB 1; Length 5173;

Mismatches 125; Conservative 0; Mismatches 77; Indels 3;

QY 703 TTCTACTTTTTTTTGTAGCTATTTACTGTCTTATTTATGTAATAAACAGTCA

Db 4952 TTGTGATAATTTGTAATTTCTTTTCTTCAATTTAATGCCAAAAGTTTGCCA

QY 763 CCAAGTGTGATTTGCTTAATTTTCCCTCATGAGAAGATATTTTGATCTCCCAA

Db 5012 TAAACATATTAATATATTTTCCCTTTTAAATAACACATTTTGT---TAAAT

QY 823 ATTTGGTATAATAATGTGAGCTGTTTGGCAACTTAAAAAATAAAAAA

Db 5069 TTCCTTTAAATAAATAATTTTAAAGCAATTTGTCCTCAATAAAAAAATAAAAAA

QY 883 AAAAAAATAAAAAAATAAAAAA 907

Db 5129 AAAAAAATAAAAAAATAAAAAA 5153

RESULT 5

US-08-267-803B-8

; Sequence 8; Application US/08267803B

; Patent No. 5834183

; GENERAL INFORMATION:

; APPLICANT: Orr, Harry T.

; APPLICANT: Rannum, Laura P.W.

; APPLICANT: Chung, Ming-Yi

; APPLICANT: Zoghbi, Huda Y.

; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

; Patent No. 5834183

; TITLE OF INVENTION: Type 1 and Method for Diagnosis

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.

; STREET: P.O. Box 581415

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55458-1415

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/267,803B

; FILING DATE: 28-JUN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

Cormack, Myra H.
 ION NUMBER: 36,602
 3/DOCKET NUMBER: 110.00030120
 IATION INFORMATION:
 3: 612-305-1217
 612-305-1228
 OR SEQ ID NO: 8:
 CHARACTERISTICS:
 10660 base pairs
 acleic acid
 IESS: single
 : linear
 ?PE: DNA

CDS
 936..3384

7.2%; Score 65.2; DB 2; Length 10660;
 ilarity 58.9%; Pred. No. 2.2e-05;
 Conservative 0; Mismatches 78; Indels 0; Gaps 0;
 AGTATTACTGACATTATGATATAAAACAAAGTCACCTTTCTCCAAAGTTGTTGC 777
 ATTTCATTATATAATAAAACAATGTTGATTCAAAATTTGAACAAAATTTGTTTAAA 10530
 TTTTTCCTCCATGAGAGATATTTTGATCTCCCAATACATTTGATTTGCTATAATAA 837
 AATTGCTGTATACCAAGTACAGTTTATTGTTTCAGTATCTGCTACTAATAATAA 10590
 GTGAGGCTGTTTGCAACTTAAACAAAAAATAAATAAATAAATAAATAAATAAATAA 897
 GTGCCAATTGCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 10650

AAAAAAA 907
 |||||
 AAAAAAA 10660

pplication US/09041886
 5872

MATION:
 Redesen, Dale E.
 Rabizadeh, Sharoz
 VENTION: Proapoptotic Peptides, Dependence
 VENTION: Polypeptides and Methods of Use
 EQUENCES: 72

NCE ADDRESS:
 : Campbell & Flores LLP
 4370 La Jolla Village Drive, Suite 700
 n Diego
 alifornia
 United States
 22

ADABLE FORM:
 PE: Floppy disk
 IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 Patent in Release #1.0, Version #1.25
 LICATION DATA:
 ON NUMBER: US/09/041,886
 TE:

ACTION:
 ENT INFORMATION:
 mpbell, Cathryn A.
 ION NUMBER: 31,815
 /DOCKET NUMBER: P-LJ 2626
 CATION INFORMATION:
 : (619) 535-9001
 (619) 535-8949
 OR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
 LENGTH: 10660 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 936..3384
 US-09-041-886-16

Query Match 7.2%; Score 65.2; DB 3; Length 10660;
 Best Local Similarity 58.9%; Pred. No. 2.2e-05;
 Matches 112; Conservative 0; Mismatches 78; Indels 0;

QY 718 TTAGCTATTACTGTACTTTATGATATAAAACAAAGTCACCTTTCTCCAAAGTTG
 DB 10471 TTATTTTCATTATTATAATAAAACAATGTTGATTCAAAATTTGAACAAAATTTG
 QY 778 TATTTTTCCTCTATGAGAGATATTTTGATCTCCCAATACATTTGATTTGCT
 DB 10531 TAAATGCTGTATACCAAGTACAGTTTATTGTTTTCAGTATACTCGTACTAAT
 QY 838 ATGTGAGGCTGTTTTCGCAAACTTAAACAAAAAATAAATAAATAAATAAATAA
 DB 10591 CAGTCCCAATTGCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA
 QY 898 AAAAAAAA 907
 DB 10651 AAAAAAAA 10660

RESULT 7

US-09-227-357-40
 ; Sequence 40, Application US/09227357
 ; Patent No. 6342581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer et al.
 ; TITLE OF INVENTION: 123 Human Secreted Proteins
 ; FILE REFERENCE: PZ010F1
 ; CURRENT APPLICATION NUMBER: US/09/227,357
 ; CURRENT FILING DATE: 1999-01-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684
 ; EARLIER FILING DATE: 1998-07-07
 ; EARLIER APPLICATION NUMBER: 60/051,926
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,793
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,925
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,929
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,803
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,732
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,931
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,932
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,916
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,930
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,918
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,920
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,733
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,795
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,919

pplication US/09738946
79701
MATION:

RESULT 9
 US-08-486-049-1
 Sequence 1, Application US/08486049
 Patent No. 6572862
 GENERAL INFORMATION:
 APPLICANT: Estes, Mary K
 APPLICANT: Jiang, Xi
 APPLICANT: Graham, David Y
 TITLE OF INVENTION: Methods and Reagents to Detect and
 TITLE OF INVENTION: Characterize No. 6572862walk and Related
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 801 Pennsylvania Ave., N.W.
 CITY: Washington, D.C.
 STATE:
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,049
 FILING DATE: June 7, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Davis, Peter
 REGISTRATION NUMBER: 36,119
 REFERENCE/DOCKET NUMBER: 311.023
 TELECOMMUNICATION INFORMATION:

```

1  RESULT 11
2  US-09-2588-016-10
3  ; Sequence 10, Application US/09258016
4  ; Patent No. 6362395
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Bachettiira W. Poovaiiah, Zhihua Liu,
7  ; APPLICANT: Shameekumar Patil, Daishuke Takezawa,
8  ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
9  ; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
10 ;
11 ; NUMBER OF SEQUENCES: 19
12 ;
13 ; CORRESPONDENCE ADDRESS:
14 ;
15 ; ADDRESSEE: Alarquist Sparkman Campbell Leigh &
16 ; ADDRESSEE: Whinston, LLP
17 ; STREET: One World Trade Center
18 ; STREET: 121 S.W. Salmon Street
19 ; STREET: Suite 1600
20 ; CITY: Portland
21 ; STATE: Oregon
22 ;

```

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CDS
6938..7573
        6.7%; Score 61; DB 4; Length 7724;
ilarity 78.5%; Pred.No. 0.00017;
Conservative 0; Mismatches 20; Indels 0; Gaps 0;

ACATTGATTTTGGGTATAAATAATGTGAGCGCTTTTTGCAAACTTAAAAAAA 874
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TCATTTAATTAGTTTAAATTAGTTTAATTGATGTTAAAMAAAAAAAAAAAA 7663
|||||
IAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907
|||||
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7696
|||||
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Application US/08655352
 /991
 INFORMATION:
 Bacheetira W. Poovaiah, Zhihua Liu,
 Shameekumar Patil, Daisuke Takezawa
 INVENTION: COMPOSITIONS AND METHODS FOR
 PREVENTION OF PRODUCTION OF MALE-STERILE PLANTS
 SEQUENCES: 19
 INVENTOR ADDRESS:
 : Klarquist Sparkman Campbell Leigh &
 : Winston, LLP
 : One World Trade Center
 : 121 S.W. Salmon Street
 : Suite 1600
 : Portland,
 : Oregon
 : United States of America
 : 97204
 ADAPTABLE FORM:
 PE: Disk, 3-1/2 inch
 IBM PC compatible
 SYSTEM: MS DOS

United States of America

204

READABLE FORM:

YPE: Disk, 3-1/2 inch

G SYSTEM: MS DOS

PLICATION DATA:

ION NUMBER: US/09/258,016

ATE:

CATION:

GENT INFORMATION:

TEPHENS JR., Donald L.

TION NUMBER: 34,022

E/DOCKET NUMBER: 4630-51994

ICATION INFORMATION:

E: (503) 226-7391

FOR SEQ ID NO: 10:

1776 base pairs

ucleic acid

NESS: double stranded

: linear

YPE: CDNA to mRNA

ION: Tobacco CcAMK cDNA and deduced amino-acid

ION: sequence

: protein-coding sequence (not including

: stop codon)

: nucleotides 20-1570

0

6.7%; Score 60.8; DB 4; Length 1776;

milarity 54.0%; Pred. No. 0.00013;

Conservative 0; Mismatches 122; Indels 5; Gaps 1;

GATGGTTCATTTCTCCCAAGGATACAAATGATATACCAACAGCATGATATAGCATAT 696

GATGAGTTCAAGCTGCTATGCAAGAGATAGTTCCTTCAAGATGATGCTCTCTTC 1557

TGATATTTCTACTTTTTTTTTTTAGCTATTACTGT-----ACTTATGATATAAACA 751

CTTCGCTCTCTTAATTAATTCCTTTATGAAATTTTGGCTCTCTTTAATTTGTAATA 1617

TCACATTTCTCCAAAGTGTATGCTATTTTCCCTATGAGAAGATATTTGATCTCC 811

CCCTAATTTCTAATATCTCTAACTTCTATGACATGCAATTTATTTTATCACT 1677

CAATACATTTGATTTTGGTATAATAATGTGAGGCTGTTTTCGAACTTAAACAAAA 871

CTCGTAAAGAGATCCTTTAAATTAATTCGGAAGCCTTTATGTTAAACAAAAA 1737

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1773

Application US/09257825B

03352

MATION:

oovaiyah, Bachettira W.

Patil, Shameekumar

Takezawa, Daisuke

ENTION: Compositions and Methods for Production of Male-Sterile Plants

CE: 4630-51993

NG DATE: 1999-02-25

ATION NUMBER: US 08/655,352

DATE: 1996-05-23

ATION NUMBER: US 60/014,743

; PRIOR FILING DATE: 1996-03-28
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 1776
 ; TYPE: DNA
 ; ORGANISM: Nicotiana tabacum
 US-09-257-825B-10

Query Match 6.7%; Score 60.8; DB 4; Length 1776;
 Best Local Similarity 54.0%; Pred. No. 0.00013;
 Matches 149; Conservative 0; Mismatches 122; Indels 5;

QY 637 TGATGGCTTCATTTCTCCCAAGGATACAAATGATATACCAACAGCATGAACTAT

Db 1498 TGAAGATTCAAGCTGCTATGCAAGAGATAGTTCCTTCAAGATGTAGTCC

QY 697 TTGTATTTCTACTTTTTTTTTTTTAGCTATTACTGT-----ACTTTATGTATA

Db 1558 TCTTCGCTCTCTTAATTAATTCCTTTATGAAATTTTGGCTCTTTAATTG

QY 752 GTCACATTTCTCCAAAGTGTATTTGCTATTTTCCCTATGAGAAGATATTTT

Db 1618 ACGCTAATTTCTAATTAATATCTCTAATTTCTATGACATGCAATTTATTTT

QY 812 CCAATACATTTGATTTTGGTATAATAATGAGGCTGTTTTCGAACTTAAAA

Db 1678 ACTCGTAAAGATCCTTTAAATTAATTCGGAAGCCTTTTATGGTAAAAA

QY 872 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907

Db 1738 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1773

RESULT 13

US-09-023-655-1081
 ; Sequence 1081, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CE

; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO
 ; STATE: CALIFORNIA

; COUNTRY: USA
 ; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:

; FILING DATE:
 ; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1081:

ARACTERISTICS:
964 base pairs
cleic acid
ESS: single
linear
SOURCE:
GENBANK
182625
81

6.7%; Score 60.4; DB 4; Length 964;
ilarity 56.6%; Pred. No. 0.00013;
Conservative 0; Mismatches 86; Indels 0; Gaps 0;
CACAAATGAAGCCACCCCAATGTTGTTCTTGGTGTGGCAAGTCATAAAGG 306
AGAGAAAATGCCAAGCTTTAAGTTCGGAGTAGCAAGATTATCAGAGG 544
TAGACATTGCTATGACAGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCC 366
GGGATGAAGCTCTCTTGACTATGATGATGAAGGAGAAAGGCTCGACTGGAGATTGAAC 604
CATTCATACGAAGAGGAGGCTATGAGAGGCAAGATTCCACCGATGCTACATT 426
AATGGCTTACGGAAGAAAGGACAGCTGATGCCAAATTCACCAAAATGCAAACT 664
TTTTGAGATTGAAT 444
TTTTTGAAGTGAATT 682

1
Publication US/0888077A

ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
VENTION: GENETIC SEQUENCES AND PROTEINS RELATED
VENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
SEQUENCES: 41

NCE ADDRESS:
: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
600 SOUTH AVENUE WEST
STFIELD

USA
90-1497
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
ASCII
LOCATION DATA:
ON NUMBER: US/08/888,077A
TE: 03-JUL-1997

ATION DATA:
ON NUMBER: US 08/592,541
TE: 26-JAN-1996
ENT INFORMATION:
LISI, THOMAS M
ION NUMBER: 36,629

/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
CATION INFORMATION:
: (908) 654-5000
(908) 654-7866
OR SEQ ID NO: 41:
ARACTERISTICS:
2205 base pairs
cleic acid
ESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2205
OTHER INFORMATION: /note= "mutTMI-TM2"
US-08-888-077A-41
Query Match 6.6%; Score 60.2; DB 3; Length 2205;
Best Local Similarity 64.3%; Pred. No. 0.00019;
Matches 83; Conservative 1; Mismatches 45; Indels 0;
QY 779 ATTTTCCCTATGAGAGATATTTTGATCTCCCCAATACATTTGATTGTTA
Db 2034 AGTTGCCNTTTTAGGAATNTTTTGGATTGGGAGCAGCATGATTGATT
QY 839 TGTGAGGCTGTTTGGCAACTTAAAAA
Db 2094 TTAAGTANTTTTACACATTGAAAAA
QY 899 AAAAAAAA 907
Db 2154 AAAAAAAA 2162

RESULT 15

US-08-749-391-1
; Sequence 1, Application US/08749391
; Patent No. 5948667
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2058 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neocallimastix patriciarum
; STRAIN: 27


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: CDS
: 301..1755

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d: April 9, 2004, 10:40:29
secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

April 9, 2004, 08:12:55 ; Search time 3215 Seconds
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US-10-015-480A-179

907
1 gagcagtgcttcgtgagc.....aaaaaaaaaaaaaaaa 907

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 55026578

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST:

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

is the number of results predicted by chance to have a
iter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
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72.4	786	14	CF593540		CF593540 AGENCOURT

5	636	70.1	643	12	BG939266	BG939266
6	625.2	68.9	943	14	CD557479	CD55747
7	618.4	68.2	690	14	CA412939	CA41293
8	600	66.2	618	12	BG939267	BG93926
9	585.2	64.5	734	10	BE874396	BE87439
10	536.4	59.1	602	13	EX485892	EX48589
11	523.4	57.7	525	9	AI271550	AI271550
12	519.8	57.3	800	14	CB959508	CB95950
13	511.8	56.4	690	9	AV700682	AV700682
14	509.4	56.2	644	12	BG896952	BG89695
15	502.2	55.4	618	14	CF794142	CF79414
16	500.2	55.1	521	9	AW082138	AW082138
17	496	54.7	496	9	AI753504	AI753504
18	473	52.1	643	14	CF792774	CF79277
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20	458.8	50.6	514	9	AA809220	AA809220
21	458.8	50.6	734	14	CB570987	CB57098
22	456.2	50.3	517	9	AV745382	AV745382
23	450.2	49.6	636	14	CA313338	CA31333
24	444	49.0	546	10	BE756310	BE75631
25	438	48.3	457	9	AI879695	AI879695
26	437	48.2	604	12	B1964616	B196461
27	419.6	46.3	469	9	AV746084	AV746084
28	418	46.2	465	9	AW081079	AW081079
29	418	46.1	673	9	AI182368	AI182368
30	389.8	43.0	748	14	CB573983	CB57398
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32	383.2	42.2	498	9	AA457921	AA45792
33	381	42.0	488	10	BE604773	BE60477
34	372.6	41.1	507	9	AV746036	AV746036
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36	370.2	40.8	959	10	BF576504	BF57650
37	369.2	40.7	646	10	BF179938	BF17993
38	368.4	40.6	619	9	AV753894	AV75389
39	366.4	40.4	550	13	EX515852	EX51585
40	363	40.0	411	9	AL709203	AL709203
41	360.8	39.8	506	10	BE850956	BE85095
42	357	39.4	861	13	BU400194	BU40019
43	356.6	39.3	922	13	BU135960	BU13596
44	356	39.3	371	9	AI264068	AI264068
45	354	39.0	354	9	AI219556	AI219556

ALIGNMENTS

RESULT 1
AF092137
LOCUS
DEFINITION Homo sapiens FK506-binding protein mRNA, complete cds.
ACCESSION AF092137
VERSION AF092137.1 GI:5138923
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 1231)
Han,Z., Song,H., Dai,M., Huang,Q., Mao,Y., Zhang,Q., Ma
Luo,M., Chen,J. and Hu,R.
Huan FK506-binding protein mRNA, complete cds
REFERENCE 2 (bases 1 to 1231)
AUTHORS Han,Z.
Direct Submission
Submitted (16-SEP-1998) Shanghai Second Medical Univers
Hospital, Shanghai Institute of Hematology, 197 Rui-Jin
Shanghai 200025, P.R. China
Location/Qualifiers
1..1231
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/tissue_type="normal pituitary"
95...753
/codon_start=1
/product="FK506-binding protein"
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/db_xref="GI:5138924"
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NCSKTSKGLLNHYDGYLAKGSKFYSCRTQNEGHPKMFVGVGVIGLDDIAMTD
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NDRLSKAEINLXLRFEKDEKPRDKSYQDAVLEDFKXNDHGDGFIKPEYNNVQ
HDEL"
        34.9%; Score 860.4; DB 11; Length 1231;
milarity 99.9%; Pred. No. 4e-102;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
AGCAGTGTCTCTGCTGGAGCGCATGCCAAAAACCATGCTATTTCTATTTCAGATTCAATGT 60
AGCAGTGTCTCTGCTGGAGCGCATGCCAAAAACCATGCTATTTCTATTTCAGATTCAATGT 122
TTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGAGACACCGA 120
TTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGAGACACCGA 182
GAAGTGAATAGAGTTTGTGATCGTCCAGAAAACTGCTCTAAGACAAGCAAGAGAGGG 180
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GACCTACTAATGCCATTATGACGGCTACCTGCTAAAGACGCTCGAAATTTCTACTG 302
AGCGGACACAAAATGAAGGCCACCCCAATGGTTTCTTCTGGTGTGGGCAAGTCAT 362
AAAGGCTAGACATTCGTATGACAGATATGTCGCCCTGGAGAAAAGCGAAAGTAGTAT 360
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CCGCTTCTATTTCATACGGAAGAGGCTATGACAGAGGCAAGATTCACCGGATGC 420
CCGCTTCTATTTCATACGGAAGAGGCTATGACAGAGGCAAGATTCACCGGATGC 482
ACATTTGATTTTGAATTTGATTTGCTGTGACCAAAAGGACCCAGGACATTTGAGAC 480
ACATTTGATTTTGAATTTGATTTGCTGTGACCAAAAGGACCCAGGACATTTGAGAC 542
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TTAGAGATATTTTAAAGAAATGACCATGATGGTGGCTTTCATTTCTCCCAAGGA 660
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TACAATGTATACCAACAGATGACATATGATATTTGATTTCTACTTTTTTTTTT 720
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TTTCCCTATGAGAGATTTTGAATCTCCCAATACATTTGATTTTGGTATAATAATG 902
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Qy 841 TGAGGCTGTTTTCGAAACTTAA 862
Db 903 TGAGGCTGTTTTCGAAACTTAA 924

RESULT 2
BI827688 800 bp mRNA linear ES:
LOCUS 603074295F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:
DEFINITION mRNA sequence.
ACCESSION BI827688
VERSION BI827688.1 GI:15939238
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collectio
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informatio
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Pate: LHAM1412 row: n column: 23
High quality sequence stop: 794.

FEATURES
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/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site
Site_2: EcoRV (destroyed); RNA source normal n
anonymous male age 27. Library is oligo-dr i
directionally cloned (EcoRV site is destroyed
cloning). Average insert size 1.3 kb, insert
0.9-3 kb. Library is normalized and enriched
full-length clones and was constructed by C.
(Invitrogen). Research Genetics tracking coo
this is a NIH_MGC Library."

ORIGIN
Query Match 75.0%; Score 679.8; DB 12; Length 800;
Best Local Similarity 98.8%; Pred. No. 9.4e-79;
Matches 738; Conservative 0; Mismatches 2; Indels 7;
Qy 1 GAGCAGTGTCTCTGAGCGCATGCCAAAAACCATGCTCTTAAGACAGCA
Db 58 GAGCAGTGTCTCTGAGCGCATGCCAAAAACCATGCTCTTAAGACAGCA
Qy 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGACACAAAAGAGAGGAG
Db 118 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGACACAAAAGAGAGGAG
Qy 121 AGAAGTGAATAAGAGTTTTCATGCTCGTCCAGAAAACTGCTCTAAGACAGCA
Db 178 AGAAGTGAATAAGAGTTTTCATGCTCGTCCAGAAAACTGCTCTAAGACAGCA
Qy 181 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTTAAAGACGGCTCGAAAT
Db 237 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTTAAAGACGGCTCGAAAT
Qy 241 CAGCCGACACAAAATGAAGGCCACCCCAATGGTTTGTTCCTGGTGGG
```

```

|||||
GCCGACACAAAATGAAGCCACCCCAATGTTTCTTCTGGTGTGGGCAAGTCAT 356
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|||||
CCCGTTTCATTTCGATACCGAAGGAGGCTAT---GAAGCGAAGATTCCACCGGATGC 473
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CATTGATTTTGGATGATGAACCTTTATGCTGTGACCAAAAGGACCGAGCATTGAGAC 533
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AGCTATTTACTGTACTTTATGTTA 800

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9909 787 bp mRNA linear EST 01-MAY-2003
 COURT_13903492 NIH_MGC_147 Homo sapiens cDNA clone
 E:30341652 5', mRNA sequence.

9909
 9909.1 GI:30284429

sapiens (human)
 sapiens
 cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 bases 1 to 787
 MGC http://mgi.nci.nih.gov/
 nial Institutes of Health, Mammalian Gene Collection (MGC)
 plished (1999)
 act: Robert Strausberg, Ph.D.
 l: cgapbs-remail.nih.gov
 e Procurement: Dr. Stefan Hansson
 a Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)
 a Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing by: Agencourt Bioscience Corporation
 e distribution: MGC clone distribution information can be
 through the I.M.A.G.E. Consortium/LLNL at:
 ://image.llnl.gov
 e: NDAM373 row: h column: 13
 quality sequence stop: 621.
 Location/Qualifiers

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1. .787
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/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"

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/note="Organ: placenta; Vector: pBluescriptR; ;
 ali-XhoI; Site_2: BamH; Oligo-dr primed using I
 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for a
 insert size 2.3 kb and normalized to ROT 5. The
 primary library enriched for full-length clones
 constructed using the Cap-trapper method (Carl
 preparation). Library constructed by M. Brown
 (NIH/NHGRI, National Institutes of Health). NC
 a NIH_MGC library."

ORIGIN

Query Match	Best Local Similarity	Score	DB 14;	Length
Matches	698;	Conservative	0;	Mismatches
				Indels
				3;
QY	1	GAGCAGTGTCTGCTGGAGCGGATGCCAAAAACCATGCAATTCATTTCAGATT		
Db	78	GAGCAGTGTCTGCTGGAGCGGATGCCAAAAACCATGCAATTCATTTCAGATT		
QY	61	TTTCTTTTCTGTTGGGCGCTTTTCTGCTCAGAGACAAAGAAAGGAGAGAC		
Db	138	TTTCTTTTCTGTTGGGCGCTTTTCTGCTCAGAGACAAAGAAAGGAGAGAC		
QY	121	AGAGTGAATAATAGAAATTTTGCATCTGTCAGAAAACTGCTCTAAGCAAGCA		
Db	198	AGAGTGAATAATAGAAATTTTGCATCTGTCAGAAAACTGCTCTAAGCAAGCA		
QY	181	AGACCTACTAAATGCCATTTATGACGCTACCTGGCTAAAGACCGGCTCGAAAT		
Db	258	AGACCTACTAAATGCCATTTATGACGCTACCTGGCTAAAGACCGGCTCGAAAT		
QY	241	CAGCGGACACAAATGAAGCCACCCCAATGTTGTTCTTGGTGTGGGCA		
Db	318	CAGCGGACACAAATGAAGCCACCCCAATGTTGTTCTTGGTGTGGGCA		
QY	301	AAAAGGCTTAGACATTTCTATGACAGATATGTGCCCTGGAGAAAGCGAAAGT		
Db	378	AAAAGGCTTAGACATTTCTATGACAGATATGTGCCCTGGAGAAAGCGAAAGT		
QY	361	ACCCCTTTCATTTGCTATACGAAAGGAGCTATGCGAGAGGCGCAAGATTCCACC		
Db	438	ACCCCTTTCATTTGCTATACGAAAGGAGCTATGCGAGAGGCGCAAGATTCCACC		
QY	421	TACATTTGATTTTGGAGTTGAACTTTATGCTGTGACCAAGGACCGAGCAT		
Db	498	TACATTTGATTTTGGAGTTGAACTTTATGCTGTGACCAAGGACCGAGCAT		
QY	481	ATTAAACAAATAGACATTTGACCAATGACAGCGAGCTCTTAAAGCCGAGATAA		
Db	558	ATTAAACAAATAGACATTTGACCAATGACAGCGAGCTCTTAAAGCCGAGATAA		
QY	541	CTTGCAAGGGAATTTGAAAAGATGAAGAGCCACGTCACAGTCATATCAGGA		
Db	618	CTTGCAAGGGAATTTGAAAAGATGAAGAGCCACGTCACAGTCATATCAGGA		
QY	601	TTTAGAAGATATTTTAAAGAAATGACCATGATGGTGGTTCATTTCT-C		
Db	678	TTTAGAAGATATTTTAAAGAAATGACCATGATGGTGGTTCATTTCTTC		
QY	660	AATACATGTATATA-CCAAACGATGAA-CTATAGCATATTTGTATTT 704		
Db	738	AATACATGTATATACCAACCCGATGAACCTATAGCATATTTGTATTT 784		

RESULT 4
 CF593540
 LOCUS
 DEFINITION
 AGENCOURT_15624003 NIH_MGC_147 Homo sapiens cDNA clone
 IMAGE:30531031 5', mRNA sequence.
 ACCESSION
 CF593540
 VERSION
 CF593540.1
 GI:36347183
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

o sapiens
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 (bases 1 to 786)
 -MGC http://mgi.nci.nih.gov/
 ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 tact: Daniela S. Gerhard, Ph.D.
 ice of Cancer Genomics
 ional Cancer Institute / NIH
 9. 31 Rm10A07 Bethesda, MD 20892
 il: cgabs-remail.nih.gov
 sue Procurement: Dr. Stefan Hansson
 NA Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)
 NA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 A sequencing by: Agencourt Bioscience Corporation
 one distribution: MGC clone distribution information can be
 nd through the I.M.A.G.E. Consortium/LNL at:
 p://image.lnl.gov
 te: NDAM621 row: c column: 08
 n quality sequence stop: 623.
 Location/Qualifiers
 1. .786
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30531031"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_147"
 /notes="Organ: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamHI; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTNN-3', size-selected for average
 insert size 2.3 kb and normalized to 10⁵. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

72.4%; Score 656.8; DB 14; Length 786;
 nilarity 99.2%; Pred. No. 8.7e-76;
 Conservative 0; Mismatches 2; Indels 4; Gaps 4;
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 AGCAGTGTCTGCTGGAGCGGATGCCAAGAACCATGCTTCTTATTCAGATTCATTGT 138
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 TCTTTTATCTGTGGGGCTTTTACTGCTCAGACACAAAGAGAGAGAGACCGCA 120
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 TCTTTTATCTGTGGGGCTTTTACTGCTCAGACACAAAGAGAGAGAGACCGCA 198
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 AAGTGAATAATAGAGTTTGATCGTCCAGAAAACTGCTTAAGACAGCAAGAGAGG 258
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 TACCTACTAAATGCCATTTATGACGGCTACCTGGCTTAAGACGGCTCGAATTCATG 240
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 TACCTACTAAATGCCATTTATGACGGCTACCTGGCTTAAGACGGCTCGAATTCATG 318
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 CCCCCTTCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGTCCACCGATGC 420
 |||||
 CCCCCTTCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGTCCACCGATGC 498
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QY 421 TACATTGATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
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 Db 499 TACATTGATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
 |||||
 QY 481 ATTAAACAAATAGACATGACCAATGACAGGAGGAGCTCTCTAAAGCCGAGATAA
 |||||
 Db 559 ATTAAACAAATAGACATGACCAATGACAGGAGGAGCTCTCTAAAGCCGAGATAA
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 QY 541 CTTGCAAGGGAATTTGAAAGAGATGAGAGCCACCTGACCAAGTCTATATCAGG
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 Db 619 CTTGCAAGGGAATTTGAAAGAGATGAGAGCCACCTGACCAAGTCTATATCAGG
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 QY 601 TTTTAGAGATA-TTTTAAAGAGATGACCAATGACATGCTGATGCTTCAATTTT
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 Db 679 TTTTAGAGATA-TTTTAAAGAGATGACCAATGACATGCTGATGCTTCAATTTT
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 QY 659 GAATCAATGTATA-CCAAACACATGAACTATAG-CATATTTTATTT 704
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 Db 739 GAATCAATGTATA-CCAAACACATGAACTATAGCCATATTTTATTT 786
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RESULT 5
 BG939266
 LOCUS
 DEFINITION cr31e10.x1 Normal Human Trabecular Bone Cells Homo sapi
 clone NHTBC_cn31e10 random, mRNA sequence.
 ACCESSION BG939266
 VERSION BG939266.1 GI:14338638
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Ho
 1 (bases 1 to 643)
 Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
 Beckstrom-Youngberg,S.M., Green,E.D., Powell,J.I., Yang
 Robey,P.G., Hotchkiss,R.N. and Franccomano,C.A.
 SGAP: The Skeletal Genome Anatomy Project
 Unpublished (1997)
 Contact: Libin Jia
 Medical Genetics Branch
 National Human Genome Research Institute
 10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267
 Tel: 301-402-4877
 Fax: 301-496-7157
 Email: libin@helix.nih.gov
 DNA Sequencing and analyses by National Institutes of H
 Intramural Sequencing Center (NISC).
 Plate: 31 row: e column: 10
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1. .843
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NHTBC_cn31e10"
 /sex="Female"
 /tissue_type="Bone"
 /cell_type="Trabecular Bone Cells"
 /lab_host="SURE"
 /clone_lib="Normal Human Trabecular Bone Cells"
 /note="Organ: Hip; Vector: pBluescript; Site 1
 Library constructed by Dr. Marian Young and Dr
 Gehron Robey (NIDCR)"

ORIGIN
 Query Match 70.1%; Score 636; DB 12; Length 643;
 Best Local Similarity 100.0%; Pred. No. 4.8e-73;
 Matches 636; Conservative 0; Mismatches 0; Indels 0;
 QY 76 GGGCCTTTTACTGCTCAGACAAAGAGGAGAGACCGAAGAGTGA
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H-EZO-bao-1-19-0-UI 3', mRNA sequence.

112939

112939.1 GI:24775590

no sapiens (human)

no sapiens

taryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 690)

(-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>).

ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

or Gene Index

ublished (1997)

ttact: Robert Strausberg, Ph.D.

il: cgapbs-re@mail.nih.gov

ssue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of

hoapedics

NA Library preparation: Dr. M. Bento Soares, University of Iowa

NA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

IA Sequencing by: Dr. M. Bento Soares, University of Iowa

one Distribution: Clone distribution information can be obtained

m Dr. M. Bento Soares, bento-soares@uiowa.edu

(primer: M13 FORWARD

YA-Yes.

Location/Qualifiers

1. .690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-EZO-bao-1-19-0-UI"

/tissue_type="Chondrosarcoma Grade II"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Chl"

/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Ch1 is a cDNA library containing the following

tissues): Chondrosarcoma Grade II. The library was

constructed according to Bonaldi, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into p773-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

TGATCAGCT.

TAG TISSUE=grade-2-chondrosarcoma

TAG_LIB=UI-H-EZO

TAG_SEQ=ATCTAATATG

milarity 68.2%; Score 618.4; DB 14; Length 690;

Conservative 98.7%; Pred. No. 8.4e-71;

Conservative 0; Mismatches 3; Indels 6; Gaps 6;

CTAAATGCCATTATGACGGCTACCTGGCTAAAGCGGCTCGAAATTTCTACTGCAGCCG 246

CTAAATGCCATTATGACGGCTACCTGGCTAAAGCGGCTCG-ATTTTACTGCAGCCG 632

ACACAAATGAGGCGACCCCAATGGTTTGTGTTGGTGGGCAAGTCATAAAGG 306

ACACAAATG-AGGCCACCCCAATGG-TTGTTCCTTGTGTTGGGCAAGTCATAAAGG 574

CTAGACATTGCTATGACAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCC 366

CTAGACATTGCTATGACAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCC 514

TCATTTGCATACGGAAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATT 426

TCATTTGCATACGGAAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATT 454

Qy 427 GATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCACGGAGCATTGAG

Db 453 GATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCACGGAGCATTGAG

Qy 487 ACAAATAGACATGACCAATGACAGGAGCTCTCTTAAAGCCGAGATAAACCTC

Db 393 ACAAATAGACATGACCAATGACAGGAGCTCTCTTAAAGCCGAGATAAACCTC

Qy 547 AAGGAATTTGAAAAGATGAGAGAGCCAGTGCAGCAAGTCATATCAGGATGCA

Db 333 AAGGAATTTGAAAAGATGAGAGAGCCAGTGCAGCAAGTCATATCAGGATGCA

Qy 607 AGATATTTTAAAGAAATGACCATGATGGTGGTTCATTTCTCCCAAG

Db 273 AGATATTTTAAAGAAATGACCATGATGGTGGTTCATTTCTCCCAAG

Qy 667 TGTATACCAACAGATGAACCTATAGCATATTTGTGATTTCTACTTTTTTTT

Db 213 TGTATACCAACAGATGAACCTATAGCATATTTGTGATTTCTACTTTTTTTT

Qy 727 TACTGTACTTTTACTATATAAACCAAGTGCATTTTCT-CCAAAGTGTATTTGC

Db 154 TACTGTACTTTTACTATATAAACCAAGTGCATTTTCTCCCAAGTGTATTTGC

Qy 786 CCTATGAGAGATATTTTGTATCT-CGCCAATACATTGATTTTGGTATAATA

Db 94 CCTATGAGAGATATTTTGTATCTCCCAATACATTGATTTTGGTATAATA

Qy 845 GCTGTTTGGCAACTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

Db 34 GCTGTTTGGCAACTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

RESULT 8

EC939267/c

LOCUS

DEFINITION

clone N17BC_cn31e10 random, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

618 bp mRNA linear EST

Normal Human Trabecular Bone Cells Homo sap

GI:14338639

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

1 (bases 1 to 618)

Jia, J.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,

Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.J., Yang

Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.

SGAP: The Skeletal Genome Anatomy Project

Unpublished (1997)

Contact: Libin Jia

Medical Genetics Branch

National Human Genome Research Institute

10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267

Tel: 301-402-4877

Fax: 301-496-7157

Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of H

Intramural Sequencing Center (NISC).

Plate: 31 row: e column: 10

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. .618

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="N17BC_cn31e10"

/sex="Female"

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/cell_type="Trabecular Bone Cells"

/lab_host="SURE"

/clone_lib="Normal Human Trabecular Bone Cells"

85892 602 bp mRNA linear EST 04-SEP-2003
 Zp86C11249_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 Zp86C11249 5', mRNA sequence.
 85892
 85892.1 GI:31949079
 no sapiens (human)
 to sapiens
 ariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 602)
 orge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
 es, H. W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
 mann, S.
 . (Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., et al.)
 ublished (2003)
 tact: MIPS
 S
 Olstaedter Landstr.1, D-85764 Neuherberg, Germany
 s is the 5' sequence of the clone insert
 ne from S. Wiemann, Molecular Genome Analysis, German Cancer
 earch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 uenced by EMBL (European Molecular Biology Laboratories,
 delberg/Germany) within the cDNA sequencing consortium of the
 man Genome Project.
 si sequence available.
 s clone (DKFZp686C11249) is available at the RZPD in Berlin.
 ase contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 lin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1. .602
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59.1%; Score 536.4; DB 13; Length 602;
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 Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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 3ACCTACTAAATGCCCATTTATGACGGCTACCTGGCTTAAAGCGGCTCGAAATTTCTACG 287
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 AGCCGGACACAAAATGAAGGCCACCCCAATGTTTGTGTTGTTGGGCAAGTCAT 347
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Db 408 ACCCCCTCTTTCATATACGAAAGGAGGCTATGTCAGAGGCAAGATTCCTCA
 QY 421 TACATTCATTTTTCAGATTGAACCTTTATGCTGTGTGACCAAGGACCAAGGAGC
 Db 468 TACATTCATTTTTCAGATTGAACCTTTATGCTGTGTGACCAAGGACCAAGGAGC
 QY 481 ATTAAACAAATAGACATGGACATATGACAGCAGCTCTCTAAAGCCGAGATAT
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 QY 541 CTTCGAAAGGGAATT 555
 Db 588 CTTCGAAAGGGAATT 602

RESULT 11
 AI271550/c
 LOCUS
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 AI271550 525 bp mRNA linear EST
 Q13007.x1 Soares NhMPu S1 Homo sapiens cDNA clone IM
 3' similar to TR:Q62446 Q62446 FK506-BINDING PROTEIN 25
 mRNA sequence.
 ACCESSION
 AI271550
 VERSION
 AI271550.1 GI:3890717
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc
 1 (bases 1 to 525)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Projec
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 This clone is available royalty-free through LNL; con
 IMAGE Consortium (info@image.llnl.gov) for further infc
 Seq primer: -400P from Gibco
 High quality sequence stop: 383.
 Location/Qualifiers
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 Site 2: Eco RI; Equal amounts of plasmid DNA f
 normalized libraries (melanocyte 2NbHM, pregna
 NDHPU, and fetal heart NDH19W) were mixed, an
 were made in vitro. Following HAP purification
 was used as tracer in a subtractive hybridizat
 reaction. The driver was PCR-amplified cDNAs f
 5,000 clones made from the same 3 libraries. T
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

ORIGIN
 Query Match 57.7%; Score 523.4; DB 9; Length 525;
 Best Local Similarity 99.8%; Pred. No. 1.7e-58;
 Matches 524; Conservative 0; Mismatches 1; Indels 0;
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9508 800 bp mRNA linear EST 29-APR-2003
COURT_13887721 NIH_MGC_147 Homo sapiens cDNA clone
E:30341701 5', mRNA sequence.

9508.1 GI:30215624

sapiens (human)

sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

bases 1 to 800)
MGC <http://mgc.nci.nih.gov/>.
onal Institutes of Health, Mammalian Gene Collection (MGC)
blished (1998)

act: Robert Strausberg, Ph.D.

1: cgapbs-r@mail.nih.gov

ue Procurement: Dr. Stefan Hansson

A Library Preparation: Michael J. Brownstein (NHGRI) with help
advice from Piero Carninci (RIKEN)

A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Agencourt Bioscience Corporation
 Distribution: MGC clone distribution information can be
 found at: <http://www.mgc.org>

d through the I.M.A.G.E. Consortium/LLNL at:

://image.11nl.gov

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quality sequence stop: 468.

Location/Qualifiers

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all-XhoI; Site 2: BamH; Oligo-dT primed using primer
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insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and

primary library enriched for full-length clones and constructed using the Cap-trapper method (Cerniakov

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brown (NIMH/NHGRI, National Institutes of Health). N a NIH MGC library."

ORIGIN

Query Match	57.3%	Score 519.8	DB 14	Length 800
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QY	121	AGAAGTGAATAATAGAAGTTTTGTCATCGTCAGAAACTGCTCTAAGCAGACGA		
DB	198	AGNAGTGAATAATAGAAGTTTTGTCATCGTCAGAAACTGCTCTAAGCAGACGA		
QY	181	AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT		
DB	258	AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT		
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DB	318	CAGCCGGACACAAATGAGGCCACCCCAATGGTTGTTCTTGGTGTGGGCG		
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DB	558	ATTTAAACAAATPAGCATGGACAATGACAGGCGAGTCTCTTAAAGCCGAGAT		
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QY	597	CAGTTTTGAAAGATATTTTTTAAGAAGAAT 625		
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RESULT 13

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ACCESSION	AV700682				
VERSION	AV700682.1	GI:10302653			
KEYWORDS	EST.				
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom				
REFERENCE	1 (bases 1 to 690)				
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Xiao,H., Guo,Q., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Hu,G., Gu,J., Chen,Z. and Han,Z.				
TITLE	Insight into hepatocellular carcinogenesis at transcript by comparing gene expression profiles of hepatocellular with those of corresponding noncancerous liver				

sc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 125106
 152456

contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 203, P. R. China
 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzgchgc.sh.cn
 This clone is available at CHGC in Shanghai.
 Location/Qualifiers
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 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

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 Conservativity 0; Mismatches 2; Indels 4; Gaps 2;

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96952

644 bp mRNA linear EST 06-NOV-2001

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 VERSION BG96952.1 GI:14307193
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn
 Sathie,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., G
 Lark,M.W.
 1 (bases 1 to 644)
 Identification and initial characterization of 5000 ex
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 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651
 .PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@sk.com
 Seq primer: T7.
 Location/Qualifiers
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 DB 422 AAAAGGCCCTAGACATTGCTATGACAGATATGTCCTCGAGAAAAAGCGAAAG
 QY 361 ACCCCCTTCTATTGCTATCGGAAAGAGGCTATGAGAGGCAAGGATTCAC
 DB 482 ACCCCCTTCTATTGCTATCGGAAAGAGGCTATGAGAGGCAAGGATTCAC
 QY 421 TACATTGATTTTGGATTTGAACTTTATGCTGTGACCAAGGACCGGAGCA

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4142 618 bp mRNA linear EST 21-OCT-2003
 4142 22 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
 4142
 4142.1 GI:37798703

scrofa (pig)

scrofa
 uyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 bases 1 to 618)
 h,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 eman,D.J., Wray,J.E. and Keefe,J.W.
 ine EST collection using a normalized library constructed from
 yos representing early developmental stages
 blished (2003)

act: Smith TPL

., ARS, US Meat Animal Research Center
 ox 166, Clay Center, NE 68933-0166, USA
 402 762 4366
 402 762 4390

l: smith@mail.marc.usda.gov
 le pass sequencing. Bases called with phred v0.020425.c and
 med with the aid of the trim_alt option. Vector identified with
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Location/Qualifiers

1. 618

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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with combined RNA from day-10, day-13,

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55.4%; Score 502.2; DB 14; Length 618;

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Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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 TTTTACGTGTGGGCGATTTTACTGCTCAGGACAAAGAGAGAGAGAGAGAGAGAGAG 135

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 GTGAAATAGAGATTTTTCATGCTCCAGAAACTGCTCTAGACAAAGCAAGAGAGAG 195

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 QY 603 TAG 605
 Db 616 TAG 618

Search completed: April 9, 2004, 10:38:56
 Job time : 3244 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004, Compugen Ltd.

leic search, using sw model

April 9, 2004, 08:30:30 ; Search time 417 Seconds
(without alignments)
8159.654 Million cell updates/sec

US-10-015-480A-179

907

1 gagcagtggtctgtgagc.....aaaaaaaaaaaaaaaaaaaaa 907

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2475585 seqs, 1875730760 residues

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ength: 0

ength: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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is the number of results predicted by chance to have a
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ived by analysis of the total score distribution.

SUMMARIES

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100.0	907	14	US-10-006-818A-179	Sequence 179, App
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100.0	907	14	US-10-015-869A-179	Sequence 179, App
100.0	907	14	US-10-012-121A-179	Sequence 179, App
100.0	907	14	US-10-006-116A-179	Sequence 179, App
100.0	907	14	US-10-006-117A-179	Sequence 179, App
100.0	907	14	US-10-017-527A-179	Sequence 179, App
100.0	907	14	US-10-013-913A-179	Sequence 179, App
100.0	907	14	US-10-007-194A-179	Sequence 179, App
100.0	907	14	US-10-013-430A-179	Sequence 179, App
100.0	907	14	US-10-011-671A-179	Sequence 179, App
100.0	907	14	US-10-012-755A-179	Sequence 179, App
100.0	907	14	US-10-015-386A-179	Sequence 179, App

16	907	100.0	907	14	US-10-011-692A-179	Sequen
17	907	100.0	907	14	US-10-006-768A-179	Sequen
18	907	100.0	907	14	US-10-017-610A-179	Sequen
19	907	100.0	907	14	US-10-006-063A-179	Sequen
20	907	100.0	907	14	US-10-020-063A-179	Sequen
21	907	100.0	907	14	US-10-015-391A-179	Sequen
22	907	100.0	907	14	US-10-017-407A-179	Sequen
23	907	100.0	907	14	US-10-011-833A-179	Sequen
24	907	100.0	907	14	US-10-006-041A-179	Sequen
25	907	100.0	907	14	US-10-015-822A-179	Sequen
26	907	100.0	907	14	US-10-015-387A-179	Sequen
27	907	100.0	907	14	US-10-006-130A-179	Sequen
28	907	100.0	907	14	US-10-006-172A-179	Sequen
29	907	100.0	907	14	US-10-017-253A-179	Sequen
30	907	100.0	907	14	US-10-015-392A-179	Sequen
31	907	100.0	907	14	US-10-017-306A-179	Sequen
32	907	100.0	907	14	US-10-017-867A-179	Sequen
33	907	100.0	907	14	US-10-012-064A-179	Sequen
34	907	100.0	907	14	US-10-013-909A-179	Sequen
35	907	100.0	907	14	US-10-015-671A-179	Sequen
36	907	100.0	907	14	US-10-015-610A-179	Sequen
37	907	100.0	907	14	US-10-012-137A-179	Sequen
38	907	100.0	907	14	US-10-012-752A-179	Sequen
39	907	100.0	907	14	US-10-012-754A-179	Sequen
40	907	100.0	907	14	US-10-013-910A-179	Sequen
41	907	100.0	907	14	US-10-013-911A-179	Sequen
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44	907	100.0	907	14	US-10-012-101B-179	Sequen
45	907	100.0	907	14	US-10-015-480A-179	Sequen

ALIGNMENTS

RESULT 1

US-09-946-374-179
; Sequence 179, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750

us-10-015-480a-179.rnpb

1	1	PRIOR APPLICATION NUMBER:	60/101471
2	2	PRIOR FILING DATE:	1998-09-23
3	3	PRIOR APPLICATION NUMBER:	60/101472
4	4	PRIOR FILING DATE:	1998-09-23
5	5	PRIOR APPLICATION NUMBER:	60/101473
6	6	PRIOR FILING DATE:	1998-09-23
7	7	PRIOR APPLICATION NUMBER:	60/101474
8	8	PRIOR FILING DATE:	1998-09-23
9	9	PRIOR APPLICATION NUMBER:	60/101475
10	10	PRIOR FILING DATE:	1998-09-23
11	11	PRIOR APPLICATION NUMBER:	60/101476
12	12	PRIOR FILING DATE:	1998-09-23
13	13	PRIOR APPLICATION NUMBER:	60/101477
14	14	PRIOR FILING DATE:	1998-09-23
15	15	PRIOR APPLICATION NUMBER:	60/101479
16	16	PRIOR FILING DATE:	1998-09-23
17	17	PRIOR APPLICATION NUMBER:	60/101738
18	18	PRIOR FILING DATE:	1998-09-24
19	19	PRIOR APPLICATION NUMBER:	60/101741
20	20	PRIOR FILING DATE:	1998-09-24
21	21	PRIOR APPLICATION NUMBER:	60/101743
22	22	PRIOR FILING DATE:	1998-09-24
23	23	PRIOR APPLICATION NUMBER:	60/101915
24	24	PRIOR FILING DATE:	1998-09-24
25	25	PRIOR APPLICATION NUMBER:	60/101916
26	26	PRIOR FILING DATE:	1998-09-24
27	27	PRIOR APPLICATION NUMBER:	60/102207
28	28	PRIOR FILING DATE:	1998-09-29
29	29	PRIOR APPLICATION NUMBER:	60/102240
30	30	PRIOR FILING DATE:	1998-09-29
31	31	PRIOR APPLICATION NUMBER:	60/102307
32	32	PRIOR FILING DATE:	1998-09-29
33	33	PRIOR APPLICATION NUMBER:	60/102330
34	34	PRIOR FILING DATE:	1998-09-30
35	35	PRIOR APPLICATION NUMBER:	60/102484
36	36	PRIOR FILING DATE:	1998-09-30
37	37	PRIOR APPLICATION NUMBER:	60/102487
38	38	PRIOR FILING DATE:	1998-09-30
39	39	PRIOR APPLICATION NUMBER:	60/102570
40	40	PRIOR FILING DATE:	1998-09-30
41	41	PRIOR APPLICATION NUMBER:	60/102571
42	42	PRIOR FILING DATE:	1998-09-30
43	43	PRIOR APPLICATION NUMBER:	60/102684
44	44	PRIOR FILING DATE:	1998-10-01
45	45	PRIOR APPLICATION NUMBER:	60/102687
46	46	PRIOR FILING DATE:	1998-10-01
47	47	PRIOR APPLICATION NUMBER:	60/102965
48	48	PRIOR FILING DATE:	1998-10-02
49	49	PRIOR APPLICATION NUMBER:	60/103258
50	50	PRIOR FILING DATE:	1998-10-06
51	51	PRIOR APPLICATION NUMBER:	60/103314
52	52	PRIOR FILING DATE:	1998-10-07
53	53	PRIOR APPLICATION NUMBER:	60/103315
54	54	PRIOR FILING DATE:	1998-10-07
55	55	PRIOR APPLICATION NUMBER:	60/103328
56	56	PRIOR FILING DATE:	1998-10-07
57	57	PRIOR APPLICATION NUMBER:	60/103395
58	58	PRIOR FILING DATE:	1998-10-07
59	59	PRIOR APPLICATION NUMBER:	60/103396
60	60	PRIOR FILING DATE:	1998-10-07
61	61	PRIOR APPLICATION NUMBER:	60/103401
62	62	PRIOR FILING DATE:	1998-10-07
63	63	PRIOR APPLICATION NUMBER:	60/103449
64	64	PRIOR FILING DATE:	1998-10-06
65	65	PRIOR APPLICATION NUMBER:	60/103633
66	66	PRIOR FILING DATE:	1998-10-08
67	67	PRIOR APPLICATION NUMBER:	60/103678
68	68	PRIOR FILING DATE:	1998-10-08
69	69	PRIOR APPLICATION NUMBER:	60/103679
70	70	PRIOR FILING DATE:	1998-10-08
71	71	PRIOR APPLICATION NUMBER:	60/103711
72	72	PRIOR FILING DATE:	1998-10-08
73	73	PRIOR APPLICATION NUMBER:	60/104257

DATE: 1998-10-14
 ATION NUMBER: 60/104987
 DATE: 1998-10-20
 ATION NUMBER: 60/105000
 DATE: 1998-10-20
 ATION NUMBER: 60/105002
 DATE: 1998-10-20
 ATION NUMBER: 60/105104
 DATE: 1998-10-21
 ATION NUMBER: 60/105169
 DATE: 1998-10-22
 ATION NUMBER: 60/105266
 DATE: 1998-10-22
 ATION NUMBER: 60/105693
 DATE: 1998-10-26
 ATION NUMBER: 60/105694
 DATE: 1998-10-26
 ATION NUMBER: 60/105807

100.0%; Score 907; DB 10; Length 907;
 ilarity 100.0%; Pred. No. 3.5e-181;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 GCAGTGTCTGCTGGAGCCGATCCAAAACCATGCTTCTTATTCAGATTCATTGT 60
 |||||
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 |||||
 TCTTTTATCTGTGGGCGCTTTTCTGCTCAGAGACAAAAGAGAGGAGCACCAG 120
 |||||
 AGTGAATAATAGAGTTTGCATGCTGCCAGAAAACCTCTTAAGACAAAGCAAGAGG 180
 |||||
 AAGTGAATAATAGAGTTTGCATGCTGCCAGAAAACCTCTTAAGACAAAGCAAGAGG 180
 |||||
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 |||||
 ACTTAAATGCCATTTATGAGCGGTACTGCTGCTAAAGACGGCTCGAAATCTACTG 240
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 |||||
 SCCGGACAAAATGAAGCCACCCCAATGTTGTTCTTCTGCTGGGCGAGTCAT 300
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 AAGGCTAGACATGCTATGACAGATATGCTGCCCTGGAGAAAAGCAAGTAGTTAT 360
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 |||||
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 TGAAGATATTTTAAAGAAATGACCATGATGTTGATGGCTTCATTTCTCCCAAGGA 660
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 TCAATGATATCAACACGATGAACTATAGCATATTTGATTTCTTACTTTTTTTT 720
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 TATTACTGTACTTTATGTATAAACAAGTCACTTTCTCCAAAGTTGATTTGCTAT 780
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Db 721 GCTATTACTGTACTTATGTATATAAAACAAAGTCACTTTTCTCCAGTTGTAT
 QY 781 TTTTCCCTTATGAGAAGATATTTTGATCTCCCAATACATTCATTTTGTGTATA
 |||||
 Db 781 TTTTCCCTTATGAGAAGATATTTTGATCTCCCAATACATTCATTTTGTGTATA
 |||||
 QY 841 TGAGGCTGTGTTGGCAAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
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 Db 841 TGAGGCTGTGTTGGCAAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
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 QY 901 AAAAAA 907
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 Db 901 AAAAAA 907
 |||||

RESULT 2
 US-10-006-856A-179
 ; Sequence 179, Application US/10006856A
 ; Publication No. US20030044841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
 ; FILE REFERENCE: P2830P1C14
 ; CURRENT APPLICATION NUMBER: US/10/006,856A
 ; NUMBER OF SEQ ID NOS: 477
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-006-856A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
 Best Local Similarity 100.0%; Pred. No. 3.5e-181;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;
 QY 1 GAGCAGTGTCTCTCGAGCCGATGCCAAAAACCATGCAATTCCTTATTCAGATT
 Db 1 GAGCAGTGTCTCTCGAGCCGATGCCAAAAACCATGCAATTCCTTATTCAGATT
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 QY 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGAGAG
 Db 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGAGAG
 |||||
 QY 121 AGAAGTGAATAATAGAAAGTTTTCATCGCTCCAGAAAACCTCTCTAAGACAGCA
 Db 121 AGAAGTGAATAATAGAAAGTTTTCATCGCTCCAGAAAACCTCTCTAAGACAGCA
 |||||
 QY 181 AGACCTTACTAAATGCCCATTTATGACGGCTACCTGGCTAAGACGGCTCGAAATTC
 Db 181 AGACCTTACTAAATGCCCATTTATGACGGCTACCTGGCTAAGACGGCTCGAAATTC
 |||||
 QY 241 CAGCGGACACAAATGAAGCCACCCCAATGTTTGTCTTGTGTTGGGCAJ
 Db 241 CAGCGGACACAAATGAAGCCACCCCAATGTTTGTCTTGTGTTGGGCAJ
 |||||
 QY 301 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCCTCGAGAAAACCGAAAGT
 |||||

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 ACCCTTCATTGTCATACGGAAGAGGCTATGACAGAGGCAAGATTCCACCGGATGC 420
 TACATTGATTTTGGAGATTGAACTTTATGCTGTGACCAAAGGACCAACGAGCATGAGAC 480
 TACATTGATTTTGGAGATTGAACTTTATGCTGTGACCAAAGGACCAACGAGCATGAGAC 480
 VTTTAAACAAATAGACATGGACATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTA 540
 VTTTAAACAAATAGACATGGACATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTA 540
 TTGCAAGGGAATTTGAAAAGATGAGAACCCACGTCACAAAGTCATATCAGGATGCAAT 600
 TTGCAAGGGAATTTGAAAAGATGAGAACCCACGTCACAAAGTCATATCAGGATGCAAT 600
 TTGAGAGATATTTTAAAGAGATGACCATGATGGTGGTATGCTCTCTCTCTCTCTCT 660
 TTGAGAGATATTTTAAAGAGATGACCATGATGGTGGTATGCTCTCTCTCTCTCTCT 660
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 TACAATGTATACCAACACGATGAACATATAGCATATTTGTTTCTCTCTCTCTCTCT 720
 CTATTTACTGTACTTTATGATATATATATATATATATATATATATATATATATAT 780
 CTATTTACTGTACTTTATGATATATATATATATATATATATATATATATATATAT 780
 TTTCCCTATGAGAAATATTTGATCTCCCAATACATGATTTTGGTATATATAAATG 840
 TTTCCCTATGAGAAATATTTGATCTCCCAATACATGATTTTGGTATATATAAATG 840
 GAGGCTGTTTGGCAACTTAAACAAATATATATATATATATATATATATATATATAT 900
 GAGGCTGTTTGGCAACTTAAACAAATATATATATATATATATATATATATATATAT 900

AAAAA 907

AAAAA 907

179 Application US/10006818A
 C. US200305406A1

WATION:

Aker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Baton, Pan L.
 Ferrara, Napoleone
 Fong, Sherman
 Bao, Wei-Qiang
 Jodard, Audrey
 Jodowski, Paul J.
 Frimaldi, Christopher J.
 Burney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.

EN10N: Secreted and Transmembrane Polypeptides and Nucleic
 EN10N: Acids Encoding the Same

CE: P2830P1C4

ICATION NUMBER: US/10/006,818A

NG DATE: 2001-12-06

ation removed - See File Wrapper or Palm

2 ID NOS: 477

US-10-006-818A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
 Best Local Similarity 100.0%; Pred. No. 3.5e-181;
 Matches 907; Conservative 0; Mismatches 0; Indels 0

Qy 1 GAGCAGTGTCTGTGTCGAGCGGATGCCAAAACCATGCATTTCTTATTCAGT
 Db 1 GAGCAGTGTCTGTGTCGAGCGGATGCCAAAACCATGCATTTCTTATTCAGT
 Qy 61 TTTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAG
 Db 61 TTTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAAGAAAGAGGAG
 Qy 121 AGAAGTGAATAGAAAGTTTGTGATCTGTCAGAAAACCTGCTTAAGACAGAGC
 Db 121 AGAAGTGAATAGAAAGTTTGTGATCTGTCAGAAAACCTGCTTAAGACAGAGC
 Qy 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAA
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 Db 361 ACCCCCTTCATTTGCTATGACAGAGGAGGCTATGACAGAGGCAAGATCCAC
 Qy 421 TACATTTGATTTTGTGATTTGAACTTTATGCTGTGACCAAGAGCACCAGGAGCA
 Db 421 TACATTTGATTTTGTGATTTGAACTTTATGCTGTGACCAAGAGCACCAGGAGCA
 Qy 481 ATTAAACAAATAGACATGACAGATGACAGGAGGCTCTCTAAAGCGAGATAP
 Db 481 ATTAAACAAATAGACATGACAGATGACAGGAGGCTCTCTAAAGCGAGATAP
 Qy 541 CTTGCAAGGGAATTTGAAAAGATGAGAACCCACGTCGACCAAGTCATATCAGG
 Db 541 CTTGCAAGGGAATTTGAAAAGATGAGAACCCACGTCGACCAAGTCATATCAGG
 Qy 601 TTTAGAGATATTTTAAAGAAATGACCATGATGATGATGCTTCTTCTTCTC
 Db 601 TTTAGAGATATTTTAAAGAAATGACCATGATGATGATGCTTCTTCTTCTC
 Qy 661 ATACATGATATACCAACAGATGAACTATAGCATATTTGCTTCTTCTTCTTCT
 Db 661 ATACATGATATACCAACAGATGAACTATAGCATATTTGCTTCTTCTTCTTCT
 Qy 721 GCTATTTACTGTACTTTTATGATAAAACAAAGTCACCTTTCTTCTTCTTCTTCT
 Db 721 GCTATTTACTGTACTTTTATGATAAAACAAAGTCACCTTTCTTCTTCTTCTTCT
 Qy 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATGATTTTGGTATA
 Db 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATGATTTTGGTATA
 Qy 841 TGAGGCTGTTTGGCAACTTAAACAAATGAAAAAAGAAAAAAGAAAAAAGAAAAA
 Db 841 TGAGGCTGTTTGGCAACTTAAACAAATGAAAAAAGAAAAAAGAAAAAAGAAAAA
 Qy 901 AAAAAA 907
 Db 901 AAAAAA 907

RESULT 4

US-10-015-393A-179

jmo sapiens

1

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mo sapiens .79

100.0%; Score 907; DB 14; Length 907;
ilarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GAGGCTGTTTGCACCTTTAAACAAACCAACCAACCAACCAACCAACCAACCA 900
AAAAA 907
AAAAA 907

179 Application US/10012121A
3. US20030073810A1
WATION:
aker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Soo, Wei-Qiang
Soddard, Audrey
Sodowski, Paul J.
Strimbold, Christopher J.
Surney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/10/012,121A
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 179
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-121A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
Best Local Similarity 100.0%; Pred. No. 3.5e-181; Indels 0;
Matches 907; Conservative 0; Mismatches 0; Indels 0;
QY 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCAATTTCTTATTCAGAT
DB 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCAATTTCTTATTCAGAT
QY 61 TTTCTTTTATCTGTTGGGCTTTTACTGCTCAGAGACAAAAAGAGAGAG
DB 61 TTTCTTTTATCTGTTGGGCTTTTACTGCTCAGAGACAAAAAGAGAGAG
QY 121 AGAAGTGAAATAGAAAGTTTTCATGCTCCAGAAAACTGCTTAAGACAGCA
DB 121 AGAAGTGAAATAGAAAGTTTTCATGCTCCAGAAAACTGCTTAAGACAGCA
QY 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
DB 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
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DB 301 AAAAGCCCTAGACATTTGCTATGACAGATATGTCCTGGAGAAAAAGCAAAAG
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DB 361 ACCCTCTTATTTGCTATGACAGATATGTCCTGGAGAAAAAGCAAAAGCAAAAG
QY 421 TACATTTGATTTTGGATTTGAACTTTATGCTGTGACCAAGGACCAAGGAGCA
DB 421 TACATTTGATTTTGGATTTGAACTTTATGCTGTGACCAAGGACCAAGGAGCA
QY 481 ATTAAACAAATAGACATGCAATGACAGGAGCTCTCTAAAGCCGAGATTA
DB 481 ATTAAACAAATAGACATGCAATGACAGGAGCTCTCTAAAGCCGAGATTA
QY 541 CTGCAAGGGAATTTGAAAAAGATGAGAAAGCAAGTGCATATCATATCAGG
DB 541 CTGCAAGGGAATTTGAAAAAGATGAGAAAGCAAGTGCATATCATATCAGG
QY 601 TTTAGAAGATATTTTAAAGAAATGACCATGATGTTGATGCTTCTTCTC
DB 601 TTTAGAAGATATTTTAAAGAAATGACCATGATGTTGATGCTTCTTCTC
QY 661 ATACAATGTATACCAACGATGAATATGATATTTGATATTTCTACTTTT
DB 661 ATACAATGTATACCAACGATGAATATGATATTTGATATTTCTACTTTT
QY 721 GCTATTTACTGTTACTTTATGATATTAAGGACCAAGTGCATTTCTC
DB 721 GCTATTTACTGTTACTTTATGATATTAAGGACCAAGTGCATTTCTC
QY 781 TTTTCCCTATGAGAGATATTTGATCTCCCAATACATTTGATTTGTTAT
DB 781 TTTTCCCTATGAGAGATATTTGATCTCCCAATACATTTGATTTGTTAT

us-10-015-480a-179.rnpb

179 Application US/10006116A
o. US20030082626A1
MATION:
aker, Kevin P.
Botstein, David
Desnoyers, Luc
Saton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Zao, Wei-Qiang
Joddard, Audrey
Jodowski, Paul J.
Primaldi, Christopher J.
Turney, Austin L.
Hillan, Kenneth J.
an, James
aoni, Nicholas F.
ENTION: Secreted and Transmembrane Polypeptides and Nucleic
ENTION: Acids Encoding the Same
E: P2830P1C15
G DATE: 2001-12-16
TION NUMBER: US/10/006,116A
TION NUMBER: 60/098716
DATE: 1998-09-01
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PRIORITY FILING DATE: 1998-09-29
PRIORITY APPLICATION NUMBER: 60/102331

us-10-015-480a-179.rnpb

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100.0%; Score 907; DB 14; Length 907;
ilarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACACGTGTTCTGCTGAGCCGATGCCAAAAACCATGCATTCTTATTCAGATTCATGT 60
ACACGTGTTCTGCTGAGCCGATGCCAAAAACCATGCATTCTTATTCAGATTCATGT 60

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QY	61	TTTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAGAAAAGAGGAG
DB	61	TTTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAGAAAAGAGGAG
QY	121	AGAAGTGAAAATAGAACTTTTGGCATCGTCAGAAAACTGCTCTAAGACAACGCG
DB	121	AGAACTGAAAATAGAACTTTTGGCATCGTCAGAAAACTGCTCTAAGACAACGCG
QY	181	AGACCTACTAAATGCGCCCATTTATGACGCTACCTGGCTAAAGACGGCTCGAAAT
DB	181	AGACCTACTAAATGCGCCCATTTATGACGCTACCTGGCTAAAGACGGCTCGAAAT
QY	241	CACCGGACACAAAATGAAGCGCACCCCAATGGTTTGTCTTGGTGTGGGCG
DB	241	CACCGGACACAAAATGAAGCGCACCCCAATGGTTTGTCTTGGTGTGGGCG
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QY	361	ACCCCTTCATTTGCATACGAAAGGAGGCTATGCAGAAAGGCGCAAGATTCCAC
DB	361	ACCCCTTCATTTGCTATACGAAAGGAGGCTATGCAGAAAGGCGCAAGATTCCAC
QY	421	TACATTGATTTTGAGATTCAACTTTATGCTGTGACCAAGAGGACCGCGAGCA
DB	421	TACATTGATTTTGAGATTGAACTTTATGCTGTGACCAAGAGGACCGCGAGCA
QY	481	ATTTAAACAATAAGACATGGACAATGACAGGCGAGCTCTCTAAAGCCGAGATAA
DB	481	ATTTAAACAATAAGACATGGACAATGACAGGCGAGCTCTCTAAAGCCGAGATAA
QY	541	CTTGCAAAAGGGAATTTGMAAAGATGAGAGGCCACCGTGACAAGTCATATCAGG
DB	541	CTTGCAAAAGGGAATTTGMAAAGATGAGAGGCCACCGTGACAAGTCATATCAGG
QY	601	TTTGAAGATATTTTAAAGAAGATGACCATGATGSGTATGGTCTCATTTCTCTC
DB	601	TTTGAAGATATTTTAAAGAAGATGACCATGATGSGTATGGTCTCATTTCTCTC
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QY	721	GCTATTACTGTACTTTATGTATATAAAACAAAGTCACCTTTTCTCCAGTTGTAT
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DB	841	TGAGGCTGTTTGGCAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
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RESULT 8
US-10-006-117A-179 ; Sequence 179, Application US10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

iao, Wei-Qiang
Jodard, Audrey
Jodowski, Paul J.
Krimaldi, Christopher J.
Lurney, Austin L.
Mullan, Kenneth J.
Pan, James
Pao, Nicholas F.
PNION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
E: P2830P1C13
CATION NUMBER: US/10/006,117A
IG DATE: 2002-03-19
tion removed - See File Wrapper or Palm
DATE: 2001-07-09
ID NOS: 477

no sapiens
79

100.0%; Score 907; DB 14; Length 907;
ilarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3 DATE: 1998-09-10
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ATION NUMBER: 60/101743
DATE: 1998-09-24
ATION NUMBER: 60/101915
DATE: 1998-09-24
ATION NUMBER: 60/101916
DATE: 1998-09-24

DATE: 1998-10-28
100.0%; Score 907; DB 14; Length 907;
milarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AGCAGTGTCTGCTGAGCGGATGCCAAAACCATGCATTTCTATTTCAGATTCATGT 60
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AAAAA 907
AAAAA 907

Sequence 179, Application US/10013913A
Publication No. US20030083462A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C40
CURRENT APPLICATION NUMBER: US/10/013,913A
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 179
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-013-913A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 907; Conservative 0; Mismatches 0; Indels 0;
QY 1 GAGCAGTGTCTGCTGAGCGGATGCCAAAACCATGCATTTCTATTTCAGAT
DB 1 GAGCAGTGTCTGCTGAGCGGATGCCAAAACCATGCATTTCTATTTCAGAT
QY 61 TTTCCTTTTATCTGCTGAGCGGCTTTTACTGCTCAGAGACAAAAGAGAGGAG
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DB 121 AGAAGTGAATAAGTGAAGTGTTCATGCTCCAGAAAACCTGCTTAAGACAAAGCA
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DB 181 AGACCTACTAAATGCCCATTTATGAGCGGCTA CTGGCTAAAGACGGCTCGAAAT
QY 241 CAGCGGACACAAAATGAAGGCCACCCCAATGTTTCTTGGTGTGGGCT
DB 241 CAGCGGACACAAAATGAAGGCCACCCCAATGTTTCTTGGTGTGGGCT
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DB 301 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCTGGAGAAAAGCGAAAAGT
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QY 421 TACATTTGATTTTGGATTTGAACTTTATGCTGTCGACCAAGGACCGAGCAT
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QY 481 ATTTAAACAATAAGACATGACATGACAGGAGCTCTCTAAAGCCGAGATAA
DB 481 ATTTAAACAATAAGACATGACATGACAGGAGCTCTCTAAAGCCGAGATAA
QY 541 CTTGCAAAAGGGAATTTGAAAAGATGAGAGGCCCGTGCAGCAAGTCATATCAGGA
DB 541 CTTGCAAAAGGGAATTTGAAAAGATGAGAGGCCCGTGCAGCAAGTCATATCAGGA

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AAAAAA 907

179
Application US/10007194A
O. US20030092061A1
MATION:
aker, Kevin P.
Botstein, David
Desnovers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
ENTION: Secreted and Transmembrane Polypeptides and Nucleic
ENTION: Acids Encoding the Same
CE: P2830P1C6
ICATION NUMBER: US/10/007,194A
NG DATE: 2002-06-25
ATION NUMBER: 60/098716
DATE: 1998-09-01
ATION NUMBER: 60/098723
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PRIORITY APPLICATION NUMBER: 60/101738
PRIORITY FILING DATE: 1998-09-24
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		Prior Filing Date: 1998-10-26	Query Match	100.0%	Score 907;	DB 14;	Length 907;
		Prior Application Number: 60/105807	Best Local Similarity	100.0%;	Pred. No. 3.5e-181;		
		Prior Filing Date: 1998-10-27	Matches 907;	Conservative 0;	Mismatches 0;	Indels 0;	
;		Prior Application Number: 60/105881					
;		Prior Filing Date: 1998-10-27					
;		Prior Application Number: 60/105882					
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;		Prior Application Number: 60/106023					
;		Prior Filing Date: 1998-10-28					
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Db	61	TTTCTTTTATCTGTPGGGCGCTTTTACTGCTCAGAGACAAAGAAAGAGGAGGA					
Qy	121	AGAGTCGAAATAGAACTTTTGATGCTCCAGAAACTGCTCTAAGCAAGCA					
Db	121	AGAGTCGAAATAGAACTTTTGATGCTCCAGAAACTGCTCTAAGCAAGCA					
Qy	181	AGACCTACTAAATGCCATATGACGCTACCTGGCTTAAGACGGCTCGAAAT					
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Db	841	TGAGCGTGTTTTGCAACTTAAAAAATAAATAAATAAATAAATAAATAAATAA					

AAAAAA 907
||||||
AAAAAA 907

179 Application US/10013430A
o. US20030092883A1

MATION:

aker, Kevin P.
Botstein, David
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

ENTION: Secreted and Transmembrane Polypeptides and Nucleic

ENTION: Acids Encoding the Same

CE: P2830P1C31

ICATION NUMBER: US/10/013,430A

NG DATE: 2002-06-25

action removed - See File Wrapper or Palm

Q ID NOS: 477

omo sapiens

179

ilarity 100.0%; Score 907; DB 14; Length 907;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

US-10-011-671A-179

; Sequence 179, Application US/10011671A

; Publication No. US20030096954A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and

; FILE REFERENCE: P2830P1C27

; CURRENT APPLICATION NUMBER: US/10/011,671A

; PRIOR FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-01

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; PRIOR APPLICATION NUMBER: 60/099536

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ATTN NUMBER: 60/106023
DATE: 1998-10-28

100.0%; Score 907; DB 14; Length 907;
milarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	841	TGAGGCTGTTTTCAAACTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Qy	901	AAAAAA 907
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RESULT 14
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; Publication No. US20030096955A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Poni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C28
; CURRENT APPLICATION NUMBER: US/10/012,755A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 179
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-755A-179

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Query Match	100.0%	Score 907;	DB 14;	Length 907;
Best Local Similarity	100.0%;	Pred. No. 3.5e-181;		
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Db	1	GAGCAGTGTTCTGCTGAGCGCGATGCCAAAAACCATGCATTTCATTTCAGAG		
Qy	61	TTTCTTTTATCTGTGGGGCCCTTTTATCTGCTCAGAGACAAAGAAAGAGGAGP		
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Qy	121	AGAAGTGAAATAGAGCTTTTGGCATCTGCAGAAAACTGTCTTAAGACAAGGP		
Db	121	AGAAGTGAAATAGAGCTTTTGGCATCTGCAGAAAACTGTCTTAAGACAAGCA		
Qy	181	AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTTAAGACGGCTCGAAT		
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Qy	241	CAGCCGGACACAAAATGAAGGCCACCCCAATATGGTTTGTCTTCGGTGTGGGC		
Db	241	CAGCCGGACACAAAATGAAGGCCACCCCAATATGGTTTGTCTTCGGTGTGGGC		
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Db	301	AAAAGGCTAGACANTGCTATGACAGATATGTGCCCTCGAGAAAGCGAAAAAG		

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AGGCTGTTTGGCAAACTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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AGGCTGTTTGGCAAACTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
|||||
AAAAA 907
|||||
AAAAA 907

```

```

79 Application US/10015386A
- US2003009625A1
NTION:
ker, Kevin P.
orstein, David
esnoyers, Luc
aton, Dan I.
errara, Napoleone
ong, Sherman
ao, Wei-Qiang
oddard, Audrey
odowski, Paul J.
rimaldi, Christopher J.
urney, Austin L.
illan, Kenneth J.
an, James
aoni, Nicholas F.
NTION: Secreted and Transmembrane Polypeptides and Nucleic
NTION: Acids Encoding the Same
E: P2830PIC55
CATION NUMBER: US/10/015,386A
G DATE: 2001-12-12
tion removed - See File Wrapper or Palm
. ID NOS: 477

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Query Match 100.0%; Score 907; DB 14; Length 907;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGATCTTCTTATTTCAGAT
DB 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGATCTTCTTATTTCAGAT
QY 61 TTTCTTTTATCTGCTGGGCGCTTTTCTGCTCAGAGACAAAGAAAGAGAGAG
DB 61 TTTCTTTTATCTGCTGGGCGCTTTTCTGCTCAGAGACAAAGAAAGAGAGAG
QY 121 AGAAGTGAATAGAAATTTTGCATGCTCCAGAAATGCTCTTAAGACAAGCA
DB 121 AGAAGTGAATAGAAATTTTGCATGCTCCAGAAATGCTCTTAAGACAAGCA
QY 181 AGACCTACTAAATGCCATTTATGAGCGCTACCTGGCTAAAGACGGCTCGAAAT
DB 181 AGACCTACTAAATGCCATTTATGAGCGCTACCTGGCTAAAGACGGCTCGAAAT
QY 241 CAGCGGACACAAATGAGAGCCACCCCAATGGTTGTTCTTGTGTGGGC
DB 241 CAGCGGACACAAATGAGAGCCACCCCAATGGTTGTTCTTGTGTGGGC
QY 301 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCTCGAGAAAGCGAAAG
DB 301 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCTCGAGAAAGCGAAAG
QY 361 ACCCGCTTCAATTCGATACGGAAGGAGGCTATGCAAGAGGCAAGATTCCAC
DB 361 ACCCGCTTCAATTCGATACGGAAGGAGGCTATGCAAGAGGCAAGATTCCAC
QY 421 TACATTTGATTTTGGAGTTGAACTTTATGCTGTCGACCAAGGACCCAGGCA
DB 421 TACATTTGATTTTGGAGTTGAACTTTATGCTGTCGACCAAGGACCCAGGCA
QY 481 ATTTAAACAAATAGACATGGAACAATGACAGGAGCTCTCTAAAGCGGAGATTA
DB 481 ATTTAAACAAATAGACATGGAACAATGACAGGAGCTCTCTAAAGCGGAGATTA
QY 541 CTTGCAAGGGAAATTTGAAAAAGATGAGAGCCACGTCGACCAAGTCATATCAGG
DB 541 CTTGCAAGGGAAATTTGAAAAAGATGAGAGCCACGTCGACCAAGTCATATCAGG
QY 601 TTTAGAGATATTTTAAAGAAATGACCATGATGGTGATGGCTTCATTTCTC
DB 601 TTTAGAGATATTTTAAAGAAATGACCATGATGGTGATGGCTTCATTTCTC
QY 661 ATACAATGTATACCAACACGATGAATATAGCATATTTGATTTTCTACTTTT
DB 661 ATACAATGTATACCAACACGATGAATATAGCATATTTGATTTTCTACTTTT
QY 721 GCTATTTACTGTAATTTATGATATTAACCAAGTCACTTTCTCAAGTTGAT
DB 721 GCTATTTACTGTAATTTATGATATTAACCAAGTCACTTTCTCAAGTTGAT
QY 781 TTTTCCCGCTATGAGAGATATTTTGTATCTCCCAATACATTTGATTTGATTA
DB 781 TTTTCCCGCTATGAGAGATATTTTGTATCTCCCAATACATTTGATTTGATTA
QY 841 TGAGGCTGTTTGGCAAACTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 841 TGAGGCTGTTTGGCAAACTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAG
QY 901 AAAAAA 907
DB 901 AAAAAA 907

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GenCore version 5.1.6
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leic search, using sw model

April 9, 2004, 07:01:20 ; Search time 480 seconds
(without alignments)
8027.324 Million cell updates/sec

US-10-015-480A-179
907
1 gagcagtggtctgtgagc.....aaaaaaaaaaaaaaaaaaaaa 907

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 6747726

ength: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- N_Geneseq_29Jan04.*
- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	907	3	AAA77672	AAA77672	Human PRO
100.0	907	3	AAA37073	AAA37073	Human PRO
100.0	907	4	AAF54329	AAF54329	DNA encod
100.0	907	4	AAC90572	AAC90572	Human PRO
100.0	907	8	ACD68366	ACD68366	Novel hum
100.0	907	8	ACH04468	ACH04468	Human cDN
100.0	907	8	ACD68012	ACD68012	Novel hum
100.0	907	9	ADC18048	ADC18048	Human PRO
100.0	907	9	ADD70694	ADD70694	Human cDN
100.0	907	9	ADD39771	ADD39771	Human cDN
100.0	907	9	ADD70217	ADD70217	Human cDN
100.0	907	9	ADD38338	ADD38338	Human cDN
100.0	907	9	ADD39294	ADD39294	Human cDN
100.0	907	9	ADD38817	ADD38817	Human cDN
100.0	907	9	ADD40248	ADD40248	Human cDN
100.0	907	9	ADE50469	ADE50469	Human cDN
100.0	907	9	ADE20081	ADE20081	Human cDN
100.0	907	9	ADE49992	ADE49992	Human cDN
100.0	907	9	ADE21550	ADE21550	Human cDN
96.9	931	7	ADA40140	ADA40140	Human sec
96.9	931	9	ADC73702	ADC73702	Human sec
96.7	971	2	AAV84433	AAV84433	Human sec
96.7	971	4	ABA83216	ABA83216	Human sec

24	877.2	95.7	971	7	ADA40497
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26	877.2	95.7	971	8	ACD44527
27	877.2	95.7	971	9	ADC73947
28	861.6	95.0	968	2	AAV84621
29	861.6	95.0	968	4	ABA83405
30	861.6	95.0	968	7	ADA40498
31	861.6	95.0	968	8	ACH04906
32	861.6	95.0	968	8	ACD44716
33	861.6	95.0	968	8	ADC73948
34	860.4	94.9	1231	3	AAA14950
35	559	61.6	761	2	AAZ11183
36	536	59.1	843	9	ADE79053
37	450	49.6	724	4	ABK43526
38	450	49.6	755	4	AAI63837
39	450	49.6	755	4	AAI63837
40	450	49.6	755	4	ABK43837
41	417	46.0	600	3	AAA44235
42	393.2	43.4	493	8	ACH33348
43	361.2	39.8	387	2	AAZ11176
C 44	335.4	37.0	464	4	AAI15004
C 45	335.4	37.0	464	4	ABA56737

ALIGNMENTS

RESULT 1
ID AAA77672 standard; cDNA; 907 BP.
XX
AC AAA77672;
XX
DT 07-NOV-2000 (first entry)
DE Human PRO1304 cDNA sequence SEQ ID NO:204.
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascular;
diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hyp
KW angiogenic; proliferative; cardiant; cardiovascular; antiather
KW cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AV, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski FU, Gurney AL, Klein RD, Kuo SS, Paoni

PR	03-NOV-1998;	98US-0106919P.	
PR	03-NOV-1998;	98US-0106932P.	
PR	03-NOV-1998;	98US-0106934P.	
PR	10-NOV-1998;	98US-0107783P.	
PR	17-NOV-1998;	98US-0108775P.	
PR	17-NOV-1998;	98US-0108779P.	
PR	17-NOV-1998;	98US-0108787P.	
PR	17-NOV-1998;	98US-0108801P.	
PR	17-NOV-1998;	98US-0108802P.	
PR	17-NOV-1998;	98US-0108806P.	
PR	17-NOV-1998;	98US-0108807P.	
PR	17-NOV-1998;	98US-0108867P.	
PR	18-NOV-1998;	98US-0108925P.	
PR	18-NOV-1998;	98US-0108948P.	
PR	18-NOV-1998;	98US-0108949P.	
PR	18-NOV-1998;	98US-0108850P.	
PR	18-NOV-1998;	98US-0108851P.	
PR	18-NOV-1998;	98US-0108852P.	
PR	18-NOV-1998;	98US-0108858P.	
PR	18-NOV-1998;	98US-0108904P.	
XX			
PA	(GETH)	GENENTECH INC.	
XX			
XX	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood		
XX	WPI; 2000-237871/20.		
DR	P-PSDB; AAY99391.		
XX			
PT	New mammalian DNA sequences encoding transmembrane, receptor or		
PT	PRO polypeptides, useful for screening of potential peptide or		
PT	molecule inhibitors of the relevant receptor/ligand interaction		
XX			
PS	Claim 2; Fig 103; 773pp; English.		
XX			
CC	AAA37022 to AAA37144 encode the new isolated human transmembran		
CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY;		
CC	transmembrane and receptor PRO proteins can be used for screen		
CC	potential peptide or small molecule inhibitors of the relevant		
CC	receptor/ligand interactions. The polypeptides and nucleotide		
CC	encoding then have various industrial applications, including t		
CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 rep		
CC	primers and hybridisation probes used in the isolation of the i		
CC	polypeptides from the present invention		
XX			
SQ	Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;		
	Query Match 100.0%; Score 907; DB 3; Length 907;		
	Best Local Similarity 100.0%; Pred. No. 2,3e-155;		
	Matches 907; Conservative 0; Mismatches 0; Indels 0;		
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Db	1	GAGCAGTGTCTCTGGAGCCGATGCCAAAAACCATGCAATTTCTTTTTCAGAT	
QY	61	TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGGAGAG	
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QY	121	AGAAGTGAATAATAGAAAGTTTTCATCGCTCCAGAAAACCTGCTCTAAGACAAGCAA	
Db	121	AGAAGTGAATAATAGAAAGTTTTCATCGCTCCAGAAAACCTGCTCTAAGACAAGCAA	
QY	181	AGACCTACTAAATGCCCATTTATGACGGCTACTGCGCTAAAGACGCGCTCGAAAT	
Db	181	AGACCTACTAAATGCCCATTTATGACGGCTACTGCGCTAAAGACGCGCTCGAAAT	
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AAAAAA 907
 |||||
 AAAAAA 907

standard; DNA; 907 BP.

1 (first entry)

ag protein of the invention #52.

transmembrane; gene therapy; ss.

ad.

1-A1.

3.

0; 2000WO-US004342.

9; 99US-0141037P.

9; 99US-0144758P.

9; 99US-0145698P.

9; 99WO-US020111.

9; 99US-0162506P.

9; 99WO-US028313.

9; 99WO-US028551.

9; 99WO-US030095.

0; 2000WO-US000219.

0; 2000WO-US000376.

(GETH) GENENTECH INC.

Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hi
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 Williams PM, Wood WI;
 WPI; 2001-071395/08.

Secreted and transmembrane proteins and nucleic acids designat
 useful as hybridization probes, in chromosome and gene mapping
 therapy.

Claim 2; Fig 103; 787pp; English.

The present invention relates to secreted and transmembrane pr
 These proteins and the DNA encoding them may be used as hybrid
 probes, in chromosome and gene mapping and in the generation o
 sense RNA and DNA. They may also be used to generate eith
 transgenic animals or knockout animals which are in turn usefu
 development and screening of therapeutically useful reagents.
 acids may also be used in gene therapy

Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Query Match 100.0%; Score 907; DB 4; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.3e-155;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGTCATTTCTTATTTCAGAT
 Db 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGTCATTTCTTATTTCAGAT

QY 61 TTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAAGAGAGAGAGA
 Db 61 TTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAAGAGAGAGAGA

QY 121 AGAAGTGAATAGAAAGTTTTCATGCTCCAGAAACTGCTCTAAGACAAGCA
 Db 121 AGAAGTGAATAGAAAGTTTTCATGCTCCAGAAACTGCTCTAAGACAAGCA

QY 181 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 Db 181 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT

QY 241 CAGCCGGACACAAAATGAAGGCCACCCCAATGGTTTGTGTTGGTGGGC
 Db 241 CAGCCGGACACAAAATGAAGGCCACCCCAATGGTTTGTGTTGGTGGGC

QY 301 AAAAGGCTTAGACATTGCTATGACAGATATGTCCTGAGAAAGCGGAAAG
 Db 301 AAAAGGCTTAGACATTGCTATGACAGATATGTCCTGAGAAAGCGGAAAG

QY 361 ACCCTCTTCAATTCGACATCGGAAAGGAGGCTATGAGAGGCAAGATTCCAC
 Db 361 ACCCTCTTCAATTCGACATCGGAAAGGAGGCTATGAGAGGCAAGATTCCAC

QY 421 TACATTTGATTTTGAAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
 Db 421 TACATTTGATTTTGAAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA

QY 481 ATTTAAACAATAGACATGGAACAATGACAGGCGAGCTCTTAAAGCGGAGATAA
 Db 481 ATTTAAACAATAGACATGGAACAATGACAGGCGAGCTCTTAAAGCGGAGATAA

QY 541 CTTGCAAGGGGAATTTGAAAAGAGATGAGAAGCCAGTGAAGAGTCAATATCAGG
 Db 541 CTTGCAAGGGGAATTTGAAAAGAGATGAGAAGCCAGTGAAGAGTCAATATCAGG

QY 601 TTTAAGAGATATTTTAAAGAGAAATGACCAATGATGGTATGCTTCAATTTCTC
 Db 601 TTTAAGAGATATTTTAAAGAGAAATGACCAATGATGGTATGCTTCAATTTCTC

andard; cDNA: 907 BP.

04 cDNA.

ဟံ့

: 2000WO-US013705.

ENTECH INC.

J, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
Godowski P, Gurney AL, Kuo SS, Mark MR, Marsters SA;
Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX	WPI; 2001-025251/03.
DR	P-PSDB; AAB50960.
XX	
PT	Seventeen nucleic acids encoding PRO polypeptides which are us
PT	diagnosis and treatment of cardiovascular, endothelial or angi
PT	disorders in a mammal.
XX	
PS	Claim 60; Fig 19; 182pp; English.
XX	
CC	The present sequence is one of seventeen nucleic acids encodin
CC	polypeptides. The PRO nucleic acids, polypeptides, agonists an
CC	antagonists are useful for treating cardiovascular, endothelia
CC	angiogenic disorders in a mammal. Examples of these disorders
CC	cardiac hypertrophy, trauma, cancer, age-related macular degen
CC	atherosclerosis, hypertension, arterial restenosis, Reynaud's (
CC	rheumatoid arthritis, angina, myocardial infarctions, thrombo
CC	and lymphangitis. The PRO polypeptides and antagonists are als
CC	prevent tumour angiogenesis and for treating periodontal disea
CC	are also used to stimulate wound healing and tissue regenerati
CC	nucleic acids, polypeptides and anti-PRO antibodies are useful
CC	diagnosing a cardiovascular, endothelial or angiogenic disease;
XX	
SQ	Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;
Query Match	100.0%; Score 907; DB 4; Length 907;
Best Local Similarity	100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;	
QY	1 GAGCAGTGTCTGCTGGAGCGCATGCACAAACCAATGCATTTCCTATTTCAGAT
Db	1 GAGCAGTGTCTGCTGGAGCGCATGCCAAAACCAATGCATTTCCTATTTCAGAT
QY	61 TTTCCTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAAGAGAGAGAG
Db	61 TTTCCTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAGAGAGAGAG
QY	121 AGAAGTGAAANTAGAAGTTTTTCATCTGCTCCAGAAAACCTCTTAAGACAAGCAJ
Db	121 AGAAGTGAAANTAGAAGTTTTTCATCTGCTCCAGAAAACCTCTCTAAGACAAGCAJ
QY	181 AGACCTCTAAATGCCATTATGACGGCTACCTGGCTAAGACGGCTCGAAAT
Db	181 AGACCTCTAAATGCCATTATGACGGCTACCTGGCTAAGACGGCTCGAAAT
QY	241 CAGCCGGACACAAAATGAAGGCCACCCCATAATGGTTGTTCTTGTTGGGGCJ
Db	241 CAGCCGGACACAAAATGAAGGCCACCCCATAATGGTTGTTCTTGTTGGGGCJ
QY	301 AAAAGGCTTAGCATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGT
Db	301 AAAAGGCTTAGCATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGT
QY	361 ACCCCCTTCATTGTGCATACGGAAGGAAGGCTATGCAGAAGGCCAAGATTCACAC
Db	361 ACCCCCTTCATTGTGCATACGGAAGGAAGGCTATGCAGAAGGCCAAGATTCACAC
QY	421 TACATGTATTTTGTAGATTGAATTTATGTCTGTGACCAAAGGACCACCGAGCAI
Db	421 TACATGTATTTTGTAGATTGAATTTATGTCTGTGACCAAAGGACCACCGAGCAJ
QY	481 ATTTTAAACAAATAGACATGGACAATGACAGCAGCTCTCTAAGCCGAGATMAJ
Db	481 ATTTTAAACAAATAGACATGGACAATGACAGCAGCTCTCTAAGCCGAGATMAJ
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Db	541 CTTCGAAAAGGGAAATTTGAAAAAGATGAGAAGCCACGTCACAAAGTCATATCAGA#
QY	601 TTTAGAAGATTTTTTAAAGAAATGACCATGTATGGTGATGCTTCATTTCTTCC
Db	601 TTTAGAAGATTTTTTAAAGAAATGACCATGTATGGTGATGCTTCATTTCTTCC

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 GAGGCTGTTTTCGAACTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 900

AAAAAA 907

|||||

AAAAAA 907

tandard; cDNA; 907 BP.

3 (first entry)

n secreted and transmembrane protein PRO1304 cDNA.

reted and transmembrane protein; PRO; angiogenesis;
 l cell proliferation; wound healing; immune response;
 tes proliferation; neonatal heart hypertrophy; tumour;
 sufficiency disorder; calcium flux; inflammation;
 endothelial growth factor-stimulated proliferation;
 kidney mesangial cell proliferation; Berger disease;
 y; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 herpeticiformis; diabetes; haemoglobin switch; insulinemia;
 beta-cell precursor cell differentiation; thalassemias;
 auditory hair cell regeneration; hearing loss; bone disorder;
 disorder; sports injury; arthritis; gene; ss.

ns.

30-A1.

3.

1; 2001US-00015869.

8; 98US-0098716P.

8; 98US-0098723P.

8; 98US-0098749P.

8; 98US-0098750P.

8; 98US-0098803P.

8; 98US-0098821P.

8; 98US-0098843P.

8; 98US-0099536P.

8; 98US-0099596P.

8; 98US-0099598P.

8; 98US-0099602P.

8; 98US-0099642P.

8; 98US-0099741P.

8; 98US-0099754P.

8; 98US-0099763P.

8; 98US-0099792P.

8; 98US-0099808P.

8; 98US-0099812P.

8; 98US-0099815P.

8; 98US-0099816P.

8; 98US-0100385P.

8; 98US-0100388P.

PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100948P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
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2000WO-US030873.
2000WO-US032678.
2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
Hard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

95293/55.
33633.

XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418;
PT PRO1787 that modulate glucose or free fatty acid uptake by ske.
PT muscle cells, and are useful for treating diabetes, hyper- or l

Query Match 100.0%; Score 907; DB 8; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;

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Db 61 TTTCTTTTATCTGTGGGSCCTTTTACTGCTCAGAGACAAAGAGAGAGAC
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QY 541 CTTGCAAGGGAATTTGAAAAAGATGAGAGGCCACGTCACAAAGTCATATCAGGA
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QY 601 TTTAGAGATATTTTAAAGAGAAATGACCATGATGGTGATGGCTTCAATTTCTCC
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QY 721 GCTATTACTGTACTTTATGATAAACAAGTCACTTTTCTCCAAAGTTGTATT
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QY 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTTGGTATAA
Db 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTTGGTATAA
QY 841 TGAGGCTGTTTTGCAAACTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA
Db 841 TGAGGCTGTTTTGCAAACTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA
QY 901 AAAAAA 907
Db 901 AAAAAA 907

tandard; cDNA; 907 BP.

13 (first entry)

1 encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; vulnery;
anidiabetic; anorectic; antihypertensive; angiogenesis; cancer;
arterial capillary; endothelial cell growth; wound healing;
T-lymphocyte proliferation; immune response suppression;
heart hypertrophy; cardiac insufficiency disorder;
endothelial growth factor; inflammation; mononuclear cell;
diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
redifferentiation; bone disorder; cartilage disorder;
ury; arthritis.

ns.

41-Al.

3.

1; 2001US-00006856.

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 3; 2000WO-US032678.
 3; 2001WO-US006520.
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 3; 2001WO-US019692.
 3; 2001WO-US021066.
 3; 2001WO-US021735.
 3; 2001US-00946374.

VENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Ildard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Imani NF, Roy MA, Smith V, Stewart TR, Tumas D, Watanabe CK, Wood WI;

92259/46.
 144486.

ited and transmembrane polypeptides and polynucleotides
 tem useful for treating various cardiac insufficiency
 bone and/or cartilage disorders such as sports injuries and

ilarity 100.0%; Score 907; DB 8; Length 907;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 781 TTTTCCCTATGAGAAAGATATTTGATCTCCCAATACATTGATTTTGGTATA
 QY 841 TGAGCTGTTTTTGCAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
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 QY 901 AAAAAA 907
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RESULT 7
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 AC ACD68012;
 XX 17-SEP-2003 (first entry)
 DT 17-SEP-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO1304 cDNA.
 DE Human; secreted and transmembrane protein; PRO; gene therapy;
 KW tissue typing; chromosome identification; vaccine; gene; ss.
 XX Homo sapiens.
 OS US2003073129-A1.
 EN 17-APR-2003.
 XX

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05-JAN-1999; 99WO-US000106.
12-APR-1999; 99US-00284291.
16-APR-1999; 99US-0129674P.
23-JUN-1999; 99US-0141037P.
20-JUL-1999; 99US-0144758P.
26-JUL-1999; 99US-0145698P.
15-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021194.
18-OCT-1999; 99US-00403297.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
16-DEC-1999; 99WO-US030095.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004342.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.

); 2000WO-US006884.
); 2000WO-US013705.
); 2000WO-US014042.
); 2000WO-US014941.
); 2000WO-US015264.
); 2000WO-US023522.
); 2000WO-US023328.
); 2000WO-US030952.
); 2000WO-US030873.
); 2000WO-US032678.
); 2001WO-US006520.
); 2001WO-US008666.
); 2001US-00872035.
); 2001WO-US017800.
); 2001US-00882636.
); 2001WO-US019692.
); 2001WO-US021066.
); 2001WO-US021735.

NENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 Idard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Jini NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 4, Wood WI;

385292/55.
 233510.

ated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
 1 of a medicament for treating a condition responsive to PRO
 3, and as therapeutic agents e.g. vaccines.

ig 103; 561pp; English.

ion describes an isolated PRO (secreted and transmembrane)
 3 (I), having at least 80% sequence identity to a sequence

ilarity 100.0%; Score 907; DB 8; Length 907;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCAGTGTCTGCTGGAGCCGATGCCAAACCATGCAATTTCTTATTCAGATTCAATCT 60

AGCAGTGTCTGCTGGAGCCGATGCCAAACCATGCAATTTCTTATTCAGATTCAATCT 60

TTCTTTTATCTGTGGGCTTTTACTGCTCAGAGACAAAGAAAGAGGAGGACACCGA 120

TTCTTTTATCTGTGGGCTTTTACTGCTCAGAGACAAAGAAAGAGGAGGACACCGA 120

HAAGTGAATAATAGAAAGTTTTCATCGTCCAGAAAACCTGCTTAAGACAAAGCAAGGAG 180

HAAGTGAATAATAGAAAGTTTTCATCGTCCAGAAAACCTGCTTAAGACAAAGCAAGGAG 180

JACCTACTAAATGCCCATATGACGGCTACCTGGCTAAAGCGGCTCGAAATTCCTACTG 240

JACCTACTAAATGCCCATATGACGGCTACCTGGCTAAAGCGGCTCGAAATTCCTACTG 240

AGCGGACACAAAATGAAGGCCACCCCAAAATGTTTCTTGTGGTGGGCAAGTCAT 300

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AAAGCCCTAGACATTGCTATGACAGATATGTCCTGGAGAAAACGCAAAAGTAGTTAT 360

AAAGCCCTAGACATTGCTATGACAGATATGTCCTGGAGAAAACGCAAAAGTAGTTAT 360

CCCCCTTCATTGCTATGAGAAAGGAGGCTATGAGAAAGGCAAGATTCCACCGATGC 420

CCCCCTTCATTGCTATGAGAAAGGAGGCTATGAGAAAGGCAAGATTCCACCGATGC 420

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ACATTGATTTTTCAGATTGAATTTTATGCTGTGACCAAGGACCAAGGAGGATTCAGAC 480

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 DB 481 ATTAAACAAATAGACATGGAATGACAGGAGCTCTCTAAAGCCGAGATAA
 QY 541 CTTGCAAGGGAATTTGAAAAAGATGAGAACCGACGTCACAGTCATATCAGG
 DB 541 CTTGCAAGGGAATTTGAAAAAGATGAGAACCGACGTCACAGTCATATCAGG
 QY 601 TTTAGAAGATATTTTAAAGAAGATGACCATGATGGTGATGGCTTCATTCTC
 DB 601 TTTAGAAGATATTTTAAAGAAGATGACCATGATGGTGATGGCTTCATTCTC
 QY 661 ATACAATGTATACCAACACGATGAACCTATAGCATATTTTGTATTCTACTTTTT
 DB 661 ATACAATGTATACCAACACGATGAACCTATAGCATATTTTGTATTCTACTTTTT
 QY 721 GCTATTACTGACTTTATGTATATAAAACAAAGTCACCTTTCTCCAAAGTTGTAT
 DB 721 GCTATTACTGACTTTATGTATATAAAACAAAGTCACCTTTCTCCAAAGTTGTAT
 QY 781 TTTTCCCTATGAGAAGATATTTTGTATCTCCCAATACATTTGATTTTGGTATA
 DB 781 TTTTCCCTATGAGAAGATATTTTGTATCTCCCAATACATTTGATTTTGGTATA
 QY 841 TGAGGCTGTTTTCGCAAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
 DB 841 TGAGGCTGTTTTCGCAAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
 QY 901 AAAAAA 907
 DB 901 AAAAAA 907

RESULT 8

ADCL8048
 ID ADC18048 standard; cDNA; 907 BP.

XX ADC18048;

XX 18-DEC-2003 (first entry)

XX Human PRO polynucleotide #52.

XX Human; PRO; gene; ss; protein electrophoresis; chromosome mapp

KW gene mapping; genetic disorder.

XX Homo sapiens.

OS US2003064925-A1.

PN 03-APR-2003.

PD 10-DEC-2001; 2001US-00013907.

PF 01-SEP-1998; 98US-0098716P.

XX 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 02-SEP-1998; 98US-0099536P.

PR 02-SEP-1998; 98US-0099596P.

PR 02-SEP-1998; 98US-0099602P.

PR 02-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

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 18; 98US-0106029P.

PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 98US-0114223P.
 PR 16-APR-1999; 98US-0129674P.
 PR 23-JUN-1999; 98US-0141037P.
 PR 20-JUL-1999; 98US-0144758P.
 PR 26-JUL-1999; 98US-0144758P.
 PR 01-SEP-1999; 98US-0145698P.
 PR 15-SEP-1999; 98US-0145698P.
 PR 29-SEP-1999; 98US-0145698P.
 PR 30-NOV-1999; 98US-0145698P.
 PR 02-DEC-1999; 98US-0145698P.
 PR 16-DEC-1999; 98US-0145698P.
 PR 05-JAN-2000; 98US-0145698P.
 PR 06-JAN-2000; 98US-0145698P.
 PR 11-FEB-2000; 98US-0145698P.
 PR 18-FEB-2000; 98US-0145698P.
 PR 24-FEB-2000; 98US-0145698P.
 PR 02-MAR-2000; 98US-0145698P.
 PR 15-MAR-2000; 98US-0145698P.
 PR 17-MAY-2000; 98US-0145698P.
 PR 22-MAY-2000; 98US-0145698P.
 PR 30-MAY-2000; 98US-0145698P.
 PR 02-JUN-2000; 98US-0145698P.
 PR 23-AUG-2000; 98US-0145698P.
 PR 24-AUG-2000; 98US-0145698P.
 PR 08-NOV-2000; 98US-0145698P.
 PR 10-NOV-2000; 98US-0145698P.
 PR 01-DEC-2000; 98US-0145698P.
 PR 28-FEB-2001; 98US-0145698P.
 PR 01-MAR-2001; 98US-0145698P.
 PR 01-JUN-2001; 98US-0145698P.
 PR 20-JUN-2001; 98US-0145698P.
 PR 29-JUN-2001; 98US-0145698P.
 PR 09-JUL-2001; 98US-0145698P.
 PR 04-SEP-2001; 98US-0145698P.

(GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, H
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H
 PI

oni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
4, Wood WI;
55602/52.
18049.

ated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
1 of a medicament for treating a condition responsive to PRO
3, and as therapeutic agents e.g. vaccines.

3Q ID NO 179; 555pp; English.

ion relates to human PRO polypeptides and the polynucleotides
hem. The sequences are useful in the preparation of a
for treating a condition responsive to a PRO polypeptide. The
as are useful in a number of functional biological assays, as
weight markers for protein electrophoresis and as therapeutic

100.0%; Score 907; DB 9; Length 907;

ilarity 100.0%; Pred. No. 2.3e-155;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCAGTGTCTGCTGAGCCGATGCCAAACCACCATGCTTCTTATTCAGATTCTTGT 60
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AGCAGTGTCTGCTGAGCCGATGCCAAACCACCATGCTTCTTATTCAGATTCTTGT 60
TCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAGAGAGAGAGACACCGA 120
|||||
TCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAGAGAGAGAGACACCGA 120
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3AAGTGAATAAGAGAGTTTGTGATCGTCCAGAAAACCTGCTTAAGACAAAGAGAGG 180
|||||
3AAGTGAATAAGAGAGTTTGTGATCGTCCAGAAAACCTGCTTAAGACAAAGAGAGG 180
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3ACCTACTAATGCCCATTTAGCGGCTACCTGGCTTAAGCGGCTCGAATTTCTACTG 240
|||||
3ACCTACTAATGCCCATTTAGCGGCTACCTGGCTTAAGCGGCTCGAATTTCTACTG 240
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AGCCGGACACAAATGAAGGGCCACCCCAATGGTTTGTCTTGTGGTGGGCAAGTCAT 300
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AGCCGGACACAAATGAAGGGCCACCCCAATGGTTTGTCTTGTGGTGGGCAAGTCAT 300
|||||
AAAGCCCTAGACATTGCTATGACAGATATGTCCTGGAGAAAACGCAAAAGTAGTTAT 360
|||||
AAAGCCCTAGACATTGCTATGACAGATATGTCCTGGAGAAAACGCAAAAGTAGTTAT 360
|||||
3CCCTTCTATTTGATAGGAAAGAGGCTATGAGAGGCAAGGATTCACCGGATGC 420
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|||||
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|||||
TATTTACTGTACTTTATGATATAAAACAAAGTCACTTTCTCCCAAGTTGTATTTGCTAT 780
|||||
TATTTACTGTACTTTATGATATAAAACAAAGTCACTTTCTCCCAAGTTGTATTTGCTAT 780
|||||

QY 781 TTTTCCCTATCAGAGATATTTTGATCTCCCAATACATTCATTTTGTGTATA
|||||
Db 781 TTTTCCCTATCAGAGATATTTTGATCTCCCAATACATTCATTTTGTGTATA
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QY 841 TCAGCTGTGTTTGCACAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
|||||
Db 841 TCAGCTGTGTTTGCACAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
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QY 901 AAAAAAA 907
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Db 901 AAAAAAA 907
|||||
RESULT 9
ADD70694
ID ADD70694 standard; cDNA; 907 BP.
XX
AC ADD70694;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1304.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage diso
KW arthritis; wound healing; diabetes; skeletal muscle cells; obe
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003099625-A1.
XX
PD 29-MAY-2003.
XX
PF 12-DEC-2001; 2001US-00015385.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099643P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
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PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.

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 98US-0114223P.
 99WO-US000106.
 99US-0129674P.
 99US-0141037P.
 99US-0144758P.
 99US-0145698P.
 99WO-US020111.
 99US-0162506P.
 99WO-US028313.
 99WO-US028551.
 99WO-US030095.
 2000WO-US000219.
 2000WO-US000376.
 2000WO-US003565.
 2000WO-US004342.
 2000WO-US005004.
 2000WO-US005841.
 2000WO-US006884.
 2000WO-US013705.
 2000WO-US014042.
 2000WO-US014941.
 2000WO-US015264.
 2000WO-US023522.
 2000WO-US023328.
 2000WO-US030952.
 2000WO-US030873.
 2000WO-US032678.
 2001WO-US006520.
 2001WO-US006666.
 2001WO-US017800.
 2001WO-US019692.
 2001WO-US021066.
 2001WO-US021735.
 2001US-00946374.
 (GETH) GENENTECH INC.
 Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 Williams PM, Wood WI;
 WPI; 2003-874602/81.
 P-PSDB; ADD70695.
 Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO141
 PRO1787 affect glucose or free fatty acid (FFA) uptake by skel
 cells and are useful for treating diabetes or hyper- or hypo-i
 Claim 2; SEQ ID NO 179; 553pp; English.
 The invention relates to an isolated PRO polypeptide (secreted
 Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.3e-155;

15-JAN-2004 (first entry)

Human cDNA encoding secreted/transmembrane protein PRO1304.

Human; ss; gene; secreted protein; transmembrane protein; PRO; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage diso arthritis; wound healing; diabetes; skeletal muscle cells; obe Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac dermatitis; herpeticiformis; Crohn's disease; thalassaemia.

Homo sapiens.

US2003083462-A1.

01-MAY-2003.

10-DEC-2001; 2001US-00013913.

05-JAN-1999; 99WO-US000106.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021194.

30-NOV-1999; 99WO-US028313.

02-DEC-1999; 99WO-US028551.

16-DEC-1999; 99WO-US030095.

05-JAN-2000; 2000WO-US000219.

06-JAN-2000; 2000WO-US000376.

11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004342.

24-FEB-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841.

15-MAR-2000; 2000WO-US006884.

17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US014941.

02-JUN-2000; 2000WO-US015264.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006866.

01-JUN-2001; 2001WO-US017800.

20-JUN-2001; 2001WO-US019692.

29-JUN-2001; 2001WO-US021066.

09-JUL-2001; 2001WO-US021735.

04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fh Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W Williams PM, Wood WI;

WPI; 2003-755122/71.

P-PSDB; ADD39772.

New secreted and transmembrane PRO polypeptides useful for treat cancers, kidney disorders, Crohn's disease, diabetes mellitus, hypo-insulinemia, sports injuries and arthritis.

Claim 2; SEQ ID NO 179; 557pp; English.

or within their associated signal peptides. Also include at least one nucleotide (NA) sequence encoding PRO, a vector comprising the host cell comprising the vector, producing PRO, a chimeric moiety comprising PRO fused to a heterologous amino acid sequence, and a nucleotide (NA) sequence encoding the heterologous amino acid sequence.

dy. Pro is useful as molecular weight markers for protein
 preis and also for chromosome identification. PRO is also
 tissue typing. PRO and PRO NA are useful as hybridisation
 a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 generating transgenic animals or knock-out animals which are
 development and screening useful reagents. PRO NA is also
 gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 les are useful for suppressing immune response. PRO1246
 le is useful for treating cardiac insufficiency disorders.
 ypeptide is also useful for treating tumours. PRO1246 and
 ypeptide are useful for stimulating calcium flux in human
 vein endothelial cells. PRO1265, PRO1250 and PRO1474
 les are useful for treating bone and/or cartilage disorders
 hritis) and wound healing. PRO1130, PRO1275 and PRO1418
 les are useful for treating diabetes in skeletal muscle cells
 y. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 lger disease or other nephropathies associated with Schonlein-
 'pura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 'PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 d PRO1575 are useful in treating thalassaemias. The present
 ncodes a PRO protein of the invention.

107 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

100.0%; Score 907; DB 9; Length 907;

milarity 100.0%; Pred. No. 2.3e-155;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGGAGCACCAGA 120

AGAGTGAATAATAGAAAGTTTTCATCTGCTCCAGAAAACCTGCTTAAGACAAAGCAAGAGGG 180

AGAGTGAATAATAGAAAGTTTTCATCTGCTCCAGAAAACCTGCTTAAGACAAAGCAAGAGGG 180

AGACTACTAAATGCCATTTATGACGGCTACCTGGCTAAAGAGCGCTCGAAAATCTACTG 240

AGACTACTAAATGCCATTTATGACGGCTACCTGGCTAAAGAGCGCTCGAAAATCTACTG 240

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AAAGGCGCTAGACATTTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTAT 360

ACCGCTTCATTTGATACGGAAGAGGAGGCTATGCAAGCAAGATTCACCGGATGC 420

ACCGCTTCATTTGATACGGAAGAGGAGGCTATGCAAGCAAGATTCACCGGATGC 420

PACATTTGATTTTGTAGATTGAACCTTTATGCTGTGACCAAGGACCCAGCGAGCATTTGACAC 480

PACATTTGATTTTGTAGATTGAACCTTTATGCTGTGACCAAGGACCCAGCGAGCATTTGACAC 480

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TTTGCAAGGGGAATTTGAAAAAGATGAGAACCCAGTGCACAGTCATATCAGGATGCAGT 600

TTTGAAGATATTTTGAAGAAATGACCATGATGCTGCTTCATTTCTCCCAAGGA 660

TTTGAAGATATTTTGAAGAAATGACCATGATGCTGCTTCATTTCTCCCAAGGA 660

Qy 661 ATACAATGTATACCAACACGATGAACATATAGCATATTTGTATTCTACTTTT
 Db 661 ATACAATGTATACCAACACGATGAACATATAGCATATTTGTATTCTACTTTT
 Qy 721 GCTATTTACTGTACTTTATGTATATATAAAACAAAGTCACATTTTCTCCAAGTTGTA
 Db 721 GCTATTTACTGTACTTTATGTATATATAAAACAAAGTCACATTTTCTCCAAGTTGTA
 Qy 781 TTTTCCCCTATGACAGATATTTTGATCTCCCCAATACATTTGATTTGGTAT
 Db 781 TTTTCCCCTATGACAGATATTTTGATCTCCCCAATACATTTGATTTGGTAT
 Qy 841 TGAGGCTGTTTTCACAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA
 Db 841 TGAGGCTGTTTTCACAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA
 Qy 901 AAAAAA 907
 Db 901 AAAAAA 907
 RESULT 11
 ADD70217
 ID ADD70217 standard; cDNA; 907 BP.
 XX
 AC ADD70217;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 Human cDNA encoding secreted/transmembrane protein PRO1304.
 Human; ss; gene; secreted protein; transmembrane protein; PRO
 immune response; cardiac insufficiency disorder; calcium flux
 umbilical vein endothelial cell; bone disorder; cartilage dis
 arthritis; wound healing; diabetes; skeletal muscle cells; ob
 Berger disease; nephropathy; Schonlein-Henoch purpura; coelia
 dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
 Homo sapiens.
 OS
 XX
 US2003054406-A1.
 XX
 20-MAR-2003.
 XX
 06-DEC-2001; 2001US-00006818.
 XX
 01-SEP-1998; 98US-0098716P.
 ER 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 01-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 ER 02-SEP-1998; 98US-0098843P.
 ER 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
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 PR 09-SEP-1998; 98US-0099602P.
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 ER 10-SEP-1998; 98US-0099741P.
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 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 ER 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 ER 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.

3: 98US-0100664P.
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 3: 98US-0108500P.
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 3: 98US-0106856P.

PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108923P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 98US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 98US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

Baker KP, Borstein D, Deanovers L, Eaton DL, Ferrara N, F
 Gao W, Goddard A, Godowski BJ, Grimaldi JC, Gurney AL, Hi
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 Williams PW, Wood RI;

WPI: 2003-708344/67.
 P-PSDB; ADD70218.

Novel isolated PRO polypeptide useful for tissue typing, modul
 PT biological activity of cell, as molecular weight markers in pr
 PT electrophoresis, for treating arthritis, tumor.

37 98US-0101738P.
 37 98US-0101741P.
 37 98US-0101915P.
 37 98US-0101916P.
 37 98US-0102207P.
 37 98US-0102240P.
 37 98US-0102307P.
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 37 98US-0108925P.
 37 98US-0108848P.
 37 98US-0108849P.
 37 98US-0108850P.
 37 98US-0108851P.
 37 98US-0108852P.

PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WL;
 XX WPI; 2003-787000/74.
 DR P-PSDB; ADD38339.

XX Novel isolated PRO polypeptide, useful for treating cancerous
 PT cardiac insufficiency disorders, wound healing, diabetes melli
 PT thalasseмии.

FS Claim 2; SEQ ID NO 179; 556pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted
 CC transmembrane protein) having at least 80% amino acid sequence

Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.3e-155;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTTCGCTGGAGCCGATGCCAAAACCATGATTTCTTATTTCAGAT
 DB 1 GAGCAGTGTTCGCTGGAGCCGATGCCAAAACCATGATTTCTTATTTCAGAT
 QY 61 TTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAAGAGAGAGA
 DB 61 TTCTTTTATCTGTGGGGCCCTTTTACTGCTCAGAGACAAAAGAGAGAGA
 QY 121 AGAAGTGAATAAGAGATTTTCATCGTCCAGAAACTGCTCTAAGACAAGCA
 DB 121 AGAAGTGAATAAGAGATTTTCATCGTCCAGAAACTGCTCTAAGACAAGCA

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AGACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTG 240
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standard; cDNA; 907 BP.

34 (first entry)

A encoding secreted/transmembrane protein PRO1304.

; gene; secreted protein; transmembrane protein; PRO; tumour;
sponse; cardiac insufficiency disorder; calcium flux;
vein endothelial cell; bone disorder; cartilage disorder;
; wound healing; diabetes; skeletal muscle cells; obesity;
sease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
s; herpetiformis; Crohn's disease; thalassaemia.

ens.

US2003096954-A1.

22-MAY-2003.

07-DEC-2001; 2001US-00011671.

XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 09-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
XX 16-SEP-1998; 98US-0100662P.
XX 16-SEP-1998; 98US-0100664P.
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XX 17-SEP-1998; 98US-0100919P.
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XX 18-SEP-1998; 98US-0100849P.
XX 18-SEP-1998; 98US-0101014P.
XX 18-SEP-1998; 98US-0101068P.
XX 18-SEP-1998; 98US-0101071P.
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20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
04-SEP-2001; 2001US-00946374.
XX
PA (GUTH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
PI Williams FM, Wood WI;
XX
DR WPI; 2003-786999/74.
DR P-PSDB; ADD39295.
XX
XX
PT Novel isolated PRO polypeptide useful for tissue typing, modul
PT biological activity of cell, as molecular weight markers in pr
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 2; SEQ ID NO 179; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted

Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Fred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;
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QY 421 TACATTGATTTTGTGAGATTGAACTTTATGCTGTGACCAAGACCAACGAGCA
DB 421 TACATTGATTTTGTGAGATTGAACTTTATGCTGTGACCAAGACCAACGAGCA

```


PA	(GETH) GENENTECH INC.
XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
PI	Williams PM, Wood WI;
XX	WPI; 2003-765477/72.
DR	P-PSDB; ADD38818.
XX	New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018,
PT	PRO1244, PRO1246, useful for treating cancerous tumors, cardia
PT	insufficiency disorders, wound healing, Crohn's disease, celia
XX	Claim 2; SEQ ID NO 179; 555pp; English.
PS	The invention relates to an isolated PRO polypeptide (secreted
CC	
	Query Match 100.0%; Score 907; DB 9; Length 907;
	Best Local Similarity 100.0%; Pred. No. 2.3e-155;
	Matches 907; Conservative 0; Mismatches 0; Indels 0;
QY	1 GAGCAGTGTCTGCTGGAGCGCATGCCAAAACATGCATTTCCTATTTCAGAT
Db	1 GAGCAGTGTCTGCTGGAGCGCATGCCAAAACATGCATTTCCTATTTCAGAT
QY	61 TTTCCTTTTACTCTGCGGGCCCTTTTACTGCTCAGAGCAAAAGAAAGAGAGAGA
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Db	121 AGAAGTGAAATAAGAAAGTTTTGTCATCGTCCAGAAAACTGCTTAAGACAAGCA
QY	181 AGACCTACTAAATGCCCATATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
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2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

VENTECH INC.

Botstein D, Deshoyers L, Eaton DL, Ferrara N, Fong S;
Idard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Jni NF, Roy MA, Smith V, Stewart RA, Tumas D, Watanabe CK;
4, Wood WI;

755104/71.
340249.

ed PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
ROI246, are useful for treating cancerous tumors and cardiac
ncy disorders.

EQ ID NO 179; 550pp; English.

ion relates to an isolated PRO polypeptide (secreted or

nilarity 100.0%; Score 907; DB 9; Length 907;
nilarity 100.0%; Pred. No. 2.3e-155;

Matches	907;	Conservative	0;	Mismatches	0;	Indels	0;
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Db	1	GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCAATTTCTTATTTCAGAT					
QY	61	TTTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAAAGAGAGAGA					
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QY	121	AGAAAGTGAAGTGAAGTTTTCATGCTCCAGAAATCTCTCTAAGACAAGCA					
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Job time : 490 secs

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us-10-015-480a-179.rge

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10/015480
Seq. IDs 179

GenCore version 5.1.6
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leic search, using sw model

April 9, 2004, 07:02:32 ; Search time 3954 Seconds
(without alignments)
9942.370 Million cell updates/sec

US-10-015-480A-179

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Minimum Match 0%

Maximum Match 100%

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score greater than or equal to the score of the result being I
and is derived by analysis of the total score distribution.

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6	861.6	95.0	968	6	BD193126	BD193126
7	762	84.0	1067	9	AF100751	AF100751
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9	667.4	73.6	669	12	BT008160	BT008160
10	651.4	71.8	666	9	AY353086	AY353086
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ALIGNMENTS

RESULT 1	AX391276	Sequence 19 from Patent WO0073445.	907 bp	DNA	linear	PAT
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DEFINITION	AX391276	Sequence 19 from Patent WO0073445.				
ACCESSION	AX391276	Sequence 19 from Patent WO0073445.				
VERSION	AX391276.1	GI:19699941				
KEYWORDS	AX391276.1	GI:19699941				
SOURCE	AX391276	Sequence 19 from Patent WO0073445.				
ORGANISM	AX391276	Sequence 19 from Patent WO0073445.				
REFERENCE	AX391276	Sequence 19 from Patent WO0073445.				
AUTHORS	AX391276	Sequence 19 from Patent WO0073445.				
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		Hom sapiens				
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		Mammalia; Euthera; Primates; Catarrhini; Hominidae; Hon				
		1				
		Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., C				
		Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marster				
		Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni,				

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motion or inhibition of angiogenesis and cardiovascularization
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entech Inc. (US)
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100.0%; Score 907; DB 6; Length 907;
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 179 from Patent WO0078961.
ACCESSION AX697111
VERSION AX697111.1 GI:29498075
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., De
Baton, D. L., Gao, W. Q., Pan, J., Botstein, D., Fong, S., Goc
Godowski, P. J., Guiney, A. L., Smith, V., Tumas, D., Wood, W.
Grimaldi, C. J., Hillan, K. J., Paoni, N. F., Roy, M. A. and We
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Genentech Inc. (US)
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P.J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
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Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Vagts,A., Wandlen,R., Watanabe,C., Wiand,D., Woods,K.,
Yanura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Wood,W.I. and Godowsky,P.
Secreted Protein Discovery Initiative (SPDI), a Large-Scale
to Identify Novel Human Secreted and Transmembrane Proteins:
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me Res. 13 (10), 2265-2270 (2003)
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X.H.F.

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eration and initial analysis of more than 15,000 full-length
an and mouse cDNA sequences
c. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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(bases 1 to 911)
ausberg,R.
ect Submission
mitted (29-JUN-2001) National Institutes of Health, Mammalian
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titute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
i-MGC Project URL: http://mgc.nci.nih.gov
tact: MGC help desk
il: cgapbs-re@mail.nih.gov
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A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Sequencing Group at the Stanford Human Genome
iter, Stanford University School of Medicine, Stanford, CA 94305
r site: http://www-sbqc.stanford.edu
tact: (Dickson, Mark) mcd@paxil.stanford.edu
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M.

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 on,P.J., Endress,G.A. and Carter,K.C.

human secreted proteins

nt: JP 2002516573-A 32 04-JUN-2002;

AN GENOME SCIENCES INC

JP 2002516573-A/32

04-JUN-2002

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 PAUL A MOORE,
 PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVI
 JIAN NI,
 PI PING PAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SO
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 PI KENNETH C CARTER
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 L.,
 ct Submission
 uted (23-OCT-1998) Rui-Jin Hospital, Shanghai Institute of
 rcinology, Molecular Medicine Center, 197, Rui-Jin Road II,
 ghai, P.R. China, 200025
 Location/Qualifiers
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84.0%; Score 762; DB 9; Length 1067;
 milarity 88.8%; Pred. No. 9.9e-132;
 Conservative 0; Mismatches 0; Indels 111; Gaps 1;
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Db 74 GAGCAGTGTCTCTGAGCCGATGCCAAAACCATGCATTTCTTTATTCAGAT
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 Db 134 TTTCTTTTATCTCTGGGCGCTTTTCTACGTCTCAGAGACAAAAGAGAGAG
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RESULT 8
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 DEFINITION BT007122
 ACCESSION BT007122
 VERSION BT007122.1 GI:30583082

Db	241	CACCCAAATGGTTTGTCTTGGTGTGGCGAAGTCATAAAAGCGCCTAGACAT
Qy	323	ACAGATATGTGCCCTGGAGAAAACGGAAGTAGTTATACCCCTTCATTTCG
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Qy	623	AATGACCATGATGGTGTATGGCTTCATTTCCTCCCAAGGAATACAATGTATACG
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Qy	683	GAACCTATAG 691
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RESULT 9	BT008160	LOCUS	669 bp	mRNA	linear	SYN
DEFINITION	Synthetic construct Homo sapiens FK506 binding protein partial cds.					
ACCESSION	BT008160	VERSION	1	GI:30585158		
KEYWORDS	F11_CDNA.					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1 (bases 1 to 669)					
AUTHORS	Kainline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Ei Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer Phelan,M. and Farmer,A.					
TITLE	Cloning of human full-length CDSs in BD Creator (TM) Sy# vector					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 669)					
AUTHORS	Kainline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Ei Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer Phelan,M. and Farmer,A.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 E Circle, Palo Alto, CA 94303, USA					
COMMENT	This CDS clone is a part of a collection of human full expression clones generated by BD Biosciences Clontech Harvard Institute of Proteomics. Each CDS has been cloned with and without stop-codon (to allow fusion with tag). The CDS has been directionally cloned using BD I cloning system between the SalI and HindIII sites of t vector. Additional sequences in the clone: 'ACC' after last codon and before HindIII site to maintain reading; ' Clone distribution: http://bioinfo.clontech.com/orfclon					
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CDNA.
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o sapiens
a ryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
malia; Euthera; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 669)
nine.N., Chen.X., Rolfs.A., Halleck.A., Hines.L., Eisenstein.S.,
ndinya.M., Raphael.J., Moreira.D., Kelley.T., LaBaer,J., Lin,Y.,
lan,M. and Farmer,A.
ning of human full-length CDSs in BD Creator(TM) System Donor
tor
ublished
(bases 1 to 669)
nine.N., Chen.X., Rolfs.A., Halleck.A., Hines.L., Eisenstein.S.,
ndinya.M., Raphael.J., Moreira.D., Kelley.T., LaBaer,J., Lin,Y.,
lan,M. and Farmer,A.
ect Submission
mitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
cle, Palo Alto, CA 94303, USA
s CDS clone is a part of a collection of human full length
ression clones generated by BD Biosciences Clontech and the
vard Institute of Proteomics. Each CDS has been cloned in two
ms: with and without stop-codon (to allow fusion with C-terminal
). The CDS has been directionally cloned using BD in-Fusion(TM)
ning system between the SalI and HindIII sites of the pDNR-DUAL
tor. Additional sequences in the clone: 'ACC' after SalI site
before 'ARG' to provide Kozak consensus sequence; 'GG' after
t codon and before HindIII site to maintain reading frame.
ne distribution: http://bioinfo.clontech.com/orfclones.
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73.8%; Score 669; DB 9; Length 669;
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Homo sapiens FK506-binding protein 7 (FKBP7) mRNA, comp
alternatively spliced.
ACCESSION AY353086
VERSION AY353086.1 GI:34099838
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 666)
AUTHORS Li,H., Zhong,G., Yu,R., Shen,C., Zhou,G., Li,M., Xiao,W
and Yang,S.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2003) Guangzhou FuluGen Co., Ltd., 5
Guangzhou Entrepreneur Park for Overseas Chinese Schola
Baoshi Rd., GETDD, Guangzhou, Guangdong 510730, China
FEATURES
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Query Match 71.8%; Score 651.4; DB 9; Length 666;
Best Local Similarity 99.4%; Pred. No. 3.7e-111; Indels 3;
Matches 665; Conservative 0; Mismatches 1;
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DB 121 CATGCTCCAGAAAACCTGCTCTAAGACAAGCAAGAGGAGAGCTACTAATATGC
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DB 361 AAGGAAGGCTAT--GAAGGCAAGATTCACCGGATGCTACATTTGATTTTGA
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36754.1 Gi:23231699

2002506615-A/8.

to sapiens (human)

to sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

malia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

o.S., Sekine.S., Kimura.T. and Nakamura.N.

(bases 1 to 761)

Human protein having transmembrane domain and DNA encoding the same

ent: JP 2002506615-A 8 05-MAR-2002;

AMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

Homo sapiens (human)

JP 2002506615-A/8

25-FEB-1999 JP 2000533542

SPISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, NOBUKO NAKAMURA PC

IN15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC

IP21/02,

C12N15/00,C12N5/00

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

Human protein having transmembrane domain

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Human protein having transmembrane domain

Human protein having transmembrane domain

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RESULT 12

AF040252

LOCUS

DEFINITION

AF040252

AF040252.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

866 bp mRNA linear RO
 Mus musculus FK506-binding protein (FKBP23) mRNA, comp
 AF040252
 AF040252.1 GI:2827254

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
 1 (bases 1 to 866)

Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam
 Honjo,T.

Molecular cloning, characterization, and chromosomal l
 of FKBP23, a novel FK506-binding protein with Ca2+-bin

Genomics 54 (1), 89-98 (1998)

99026129

9806833

2 (bases 1 to 866)

Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam
 Honjo,T.

Direct Submission

Submitted (29-DEC-1997) Center for Molecular Biology a

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BC032961			
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VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
STRABERG R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., S. Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., H. Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Ho. Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schreitz, T.E., Brownstein, M.J., Usdin, T.B., Toehnyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Pet. Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs. Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S. Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D. Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
TITLE			
JOURNAL			
MEDLINE			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			

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25937 171621 bp DNA linear PRI 29-APR-2002
 25937 AC015624
 25937.2 GI:20336792

sapiens (human)
 sapiens
 aryoza; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 171621)
 I.R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 aphimachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
 gen, E.D.

Submitted
 (bases 1 to 171621)
 I.R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
 Submitted
 nitted (11-JAN-2002) Genome Center, University of Washington,
 352145 Seattle, WA 98195, USA
 (bases 1 to 171621)
 I.R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 aphimachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
 gen, E.D.

Submitted
 nitted (29-APR-2002) Genome Center, University of Washington,
 352145 Seattle, WA 98195, USA
 Apr 29, 2002 this sequence version replaced gi:18129414.

Genome Center
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgctgs@u.washington.edu
 Drafting Center: BCM

Project Information
 Center project name: Chr-3
 Center clone name: RP11-45J19 (bc0746)
 Summary Statistics
 Sequencing vector: plasmid; 100% of reads
 Chemistry: Dye-terminator ET; 58% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 171560 bases at least Q40
 Consensus quality: 171616 bases at least Q30
 Consensus quality: 171620 bases at least Q20
 Insert size: 171621; sum-of-contigs
 Quality coverage: 7.8x in Q20 bases; sum-of-contigs

Overlapping Sequences:
 5': Mapping in progress
 3': AF000497

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible in GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise all regions were either double-stranded or sequenced with alternate chemistry or covered by high quality data (i. quality >= 30); an attempt was made to resolve all sequence problems, such as compressions and repeats; all regions covered by at least one plasmid subclone or more than c subclone; and the assembly was confirmed by restriction

Sequence Validation:

This sequence has been validated by Multiple Complete fingerprinting. Comparison of the experimentally derived fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both vector, in order to accurately represent the entire c. Small fragments below a variable cutoff (approximately are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Unique fragments are separated by dashed lines.

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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5713	5978	12408	12069	1888	1911
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Query Match 37.0%; Score 335.4; DB 9; Length 1716;
Best Local Similarity 99.7%; Pred. No. 8.7e-53;
Matches 336; Conservative 0; Mismatches 1; Indels 0

QY 526 CGAGATAAACCTCTACTTGTGCAAGGGAATTTGAAAAAGATGAGAAGCCACGT
Db 152518 CCAGATAAACCTCTACTTGTGCAAGGGAATTTGAAAAAGATGAGAAGCCACGT
QY 586 ATATCAGATGCGAGTCTTTAGAGATATTTTAAAGAGATGACCATGATGCT
Db 152458 ATATCAGATGCGAGTCTTTAGAGATATTTTAAAGAGATGACCATGATGCT
QY 646 CATTTCTCCCAAGGAATACATGTATACCAACAGATGAATATAGCATATTT
Db 152398 CATTTCTCCCAAGGAATACATGTATACCAACAGATGAATATAGCATATTT
QY 706 TACTTTTTTTTTTAGCTATTTTACTGTACTGTATGTATATAAACAAGTCAC
Db 152338 TACTTTTTTTTTTAGCTATTTTACTGTACTGTATGTATATAAACAAGTCAC
QY 766 AGTTGTATTTTGCTATTTTCCCTATGAGAGATATTTTGATCTCCCAATA
Db 152278 AGTTGTATTTTGCTATTTTCCCTATGAGAGATATTTTGATCTCCCAATA
QY 826 TTGTATAATAAATGTGAGGCTGTTTTCGAACTTAA 862
Db 152218 TTGTATAATAAATGTGAGGCTGTTTTCGAACTTAA 152182

Search completed: April 9, 2004, 09:44:48
Job time : 3965 secs

GenCore version 5.1.6
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cleic search, using frame_plus_p2n model

April 9, 2004, 09:45:16 ; Search time 3751 Seconds
(without alignments)
2565.224 Million cell updates/sec

US-10-015-480a-180

1189
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 6940544

length: 0
length: 2000000000

: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	1189	100.0	907	9	AY359015	AY359015	AY359015
6	1189	100.0	911	9	BC009711	BC009711	BC009711
7	1189	100.0	971	6	BD192938	BD192938	BD192938
8	1176	98.9	968	6	BD193126	BD193126	BD193126
9	1168.5	98.3	666	9	AY353086	AY353086	AY353086
10	1160.5	97.6	1067	9	AF100751	AF100751	AF100751
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ALIGNMENTS

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 (bases 1 to 669)
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 lan,M. and Farmer,A.
 ning of human full-length CDSs in BD Creator(TM) System Donor
 :tor
 ublished
 (bases 1 to 669)
 nine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
 indinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
 lan,M. and Farmer,A.
 :ect Submission
 mitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
 :cle, Palo Alto, CA 94303, USA
 .s CDS clone is a part of a collection of human full length
 :ression clones generated by BD Biosciences Clontech and the
 :vard Institute of Proteomics. Each CDS has been cloned in two
 :ms: with and without stop-codon (to allow fusion with C-terminal
 :). The CDS has been directionally cloned using BD In-Fusion(TM)
 :ning system between the Sali' and HindIII sites of the pDNR-DUAL
 :tor. Additional sequences in the clone: 'ACC' after Sali site
 : before 'ATG' to provide Kozak consensus sequence; 'GG' after
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 :ne distribution: http://bioinfo.clontech.com/orfclones.
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 Db 481 AATGACAGCGCAGCTCTCTAAGCGGAGATAAACCTTACTTGCAGAGGAAT
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 partial cds.
 ACCESSION BT008160
 VERSION BT008160.1 GI:30585158
 KEYWORDS FLI_CDNA.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 669)
 AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., E
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBae
 Pheian,M. and Farmer,A.
 Cloning of human full-length CDSs in BD Creator(TM) Sy
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 Unpublished
 2 (bases 1 to 669)
 Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., E
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBae
 Pheian,M. and Farmer,A.
 Direct Submission
 Submitted (13-MAY-2003) BD Biosciences Clontech, 1020
 Circle, Palo Alto, CA 94303, USA
 This CDS clone is a part of a collection of human full
 expression clones generated by BD Biosciences Clontech
 Harvard Institute of Proteomics. Each CDS has been clon
 forms: with and without stop-codon (to allow fusion with
 tag). The CDS has been directionally cloned using BD
 cloning system between the Sali' and HindIII sites of
 vector. Additional sequences in the clone: 'ACC' after

before 'ATG' to provide Kozak consensus sequence; 'GG' after
t codon and before HindIII site to maintain reading frame.
ne distribution: <http://bioinfo.clontech.com/orfclones>.

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VERSION AX391276.1 GI:19699941
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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1 Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J.,
Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marste
Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni
Watanabe, C.K.
Promotion or inhibition of angiogenesis and cardiovascular
Patent: WO 0073445-A 19 07-DEC-2000;
Genentech Inc. (US)
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 Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y.,
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 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,
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 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a La
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 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)
 JOURNAL
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 Clark,H.F.
 DIRECT SUBMISSION
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ACCESSION
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VERSION
BC009711.1 GI:16307243
KEYWORDS
MGC.
SOURCE
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ORGANISM
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., S
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., H
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hc
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Pet
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Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalcius,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (200
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AUTHORS
Strausberg,R.
DIRECT SUBMISSION
Submitted (29-JUN-2001) National Institutes of Health,
Gene Collection (MGC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20
USA
REMARK
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Contact: MGC help desk
Email: gcgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Sequencing Group at the Stanford Hum
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Web site: http://www-ahgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A.,
R. M.
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through the I.M.A.G.E. Consortium/LLNL at: http://image
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AUTHORS	Young,P., Greene,J.M., Ferrrie,A.M., Ruben,S.M., Rosen,	
	Hu,J.S., Olsen,H.S., Ebner,L.A., Brewer,L.A., Moore,P.A.,	
	Flurence,C., Florence,K., Lafleur,D.W., Ni,J., Fan,P.,	
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	PI ROSEN,	
	PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE	
	PI PAUL A MOORE,	
	PI YANGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAV	

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ZHIZHEN ZENG,
HUA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI
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KENNETH C CARTER
A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC
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arity: 100.00% Mismatches: 0
100.00% Indels: 0
6 Gaps: 0

L80 (1-222) x BD192938 (1-971)

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LOCUS 207 human secreted proteins.
DEFINITION 207 human secreted proteins.
ACCESSION BD193126
VERSION BD193126.1 GI:33002865
KEYWORDS JP 2002516573-A/220.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 968)
AUTHORS Young, P., Greene, H.S., Ferrie, A.M., Ruben, S.M., Rosen, C.
Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A.,
Florence, C., Florence, K., Lafleur, D.W., Ni, J., Pan, P.,
Fischer, C.H., Soppet, D.R., Li, Y., Ze, Z., Kyaw, H., Yu, G.
Dillon, P.J., Endress, G.A. and Carter, K.C.
207 human secreted proteins
Patent: JP 2002516573-A 220 04-JUN-2002;
HUMAN GENOME SCIENCES INC
PN JP 2002516573-A/220
PD 04-JUN-2002
PR 04-JUN-1998 JP 199502815 60/048915, 06-JUN-1997 US 60/0
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18-DEC-1997 US 60/070923
PI PAUL YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUB
PI ROSEN,
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE
PI PAUL A MOORE,
PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVI
PI JIAN NI,
PI PING PAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SO
PI ZHIZHEN ZENG,
PI HUA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, G
ENDRESS,

KENNETH C CARTER
A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC
2N5/06, C12N15/00,
C12N15/06, C12N15/09, C12N15/10, C12N15/11, G01N33/53 CC
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Key Location/Qualifiers.
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6 Gaps: 0

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ACCESSION	AY353086				
VERSION	AY353086.1	GI:34099838			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut				
	Mammalia; Eutheria; Primates; Catarrhini; Homi				
AUTHORS	Li, H., Zhong, G., Yu, R., Shen, C., Zhou, G., Li, M., Xiao, Y				
TITLE	Direct Submission				
JOURNAL	Submitted (29-JUL-2003) Guangzhou Fulenden Co., Ltd.,				
	Guangzhou Entrepreneur Park for Overseas Chinese Schol				
	BaoShi Rd., GETDD, Guangzhou, Guangdong 510730, China				
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ORIGIN					
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Percent Similarity:	99.10%	Mismatches:	1		
Best Local Similarity:	98.28%	Indels:	1		
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DB:	9				
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00751 GI:5410287

CDNA

sapiens (human)

sapiens

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(bases 1 to 1067)

n.Z., Zhang Q., Dai, M., Song, H., Mao, Y., Wu, X., Mao, M., Fu, G.,
 M., Chen, J. and Hu, R.

an FK506-binding Protein (FKBP23)-isoform gene

published

(bases 1 to 1067)

n.Z.

ect. Submission

mitted (23-OCT-1998) Rui-Jin Hospital, Shanghai Institute of
 oocrinology, Molecular Medicine Center, 197, Rui-Jin Road II,
 nghai, P.R. China, 200025

Location/Qualifiers

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 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., F
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., F

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 ac. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 ausberg,R.
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 e Collection (MGC), Cancer Genomics Office, National Cancer
 stitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 i-MGC Project URL: <http://mgc.nci.nih.gov>

il: cgapbs-remail.nih.gov
 ssue Procurement: Marcello Bento Soares, Ph.D.
 NA Library Preparation: M. Bento Soares, University of Iowa
 NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 p://www.systemsbio.org
 ctact: amadane@systemsbio.org
 p Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
 an, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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 QY 185 ArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLysAsnA
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 QY 205 GlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAspGluL
 Db 642 GGAGAGCGCTTCATTTCTCTTACGAATACAAATGTGCACCAACATGATGAGC
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 VERSION
 KEYWORDS Mus musculus (house mouse)
 SOURCE
 ORGANISM
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
 1 (bases 1 to 866)
 Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam

hisargProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
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 LysGluGlyTyr-AlaGluGlyLysIleProAspAlaThrLeuIlePheGluIleG1 140
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 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 o.S., Sekine,S., Kimura,T. and Nakamura,N.
 nan protein having transmembrane domain and DNA encoding the same
 -ent: JP 2002506615-A 1 05-MAR-2002;
 JAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
 Homo sapiens (human)
 JP 2002506615-A/1
 05-MAR-2002
 25-FEB-1999 JP 2000533542
 SISHI KATO,SHINGO SEKINE,TOMOKO KIMURA,NOBUKO NAKAMURA PC
 2N15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
 2221/02.
 C12N15/00,C12N5/00
 Human protein having transmembrane domain
 a DNA encoding the
 same
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 /organism='Homo sapiens (human)'.
 Location/Qualifiers

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 /mol_type='genomic DNA'
 /db_xref='taxon:9606'
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 Score: 653.00 Conservatives: 0
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 Best Local Similarity: 100.00% Indels: 0
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 US-10-015-480A-180 (1-222) x BD136747 (1-387)
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 Db 1 ATGCAATTCCTTATTCAGATTCATTGTTTCTTTTATCTGTGGGCGCTTTTA
 Qy 25 ArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeuHisAla
 Db 61 AGACAAAGAAAGAGGAGGAGCACCAGAAAGAGTGAATAGAGTTTGCATC
 Qy 45 AsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyrAspG
 Db 121 AACTGCTTAAGCAAGCAAGAGGAGGACCTACTAAATGCCCATTAAGCG
 Qy 65 AlalysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisP
 Db 181 GCTAAAGACGCTCGAAATTCCTACTGACGGCGGACACAAATGAAGGCCAC
 Qy 85 PheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMetThrA
 Db 241 TTTGTTCTTGTGTGGCAAGTCTATAAAGGCCCTAGACATTGCTATGACAG
 Qy 105 ProGlyGluLysArgLysValValIleProProSerPheAlaTyrGlyLysG
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 DEFINITION Mus musculus cDNA sequence BC029109, mRNA (cDNA clone 1
 IMAGE:3985764), complete cds.
 ACCESSION BC029109
 VERSION BC029109.1 GI:22137712
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Eu
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 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., H
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.
 Scheetz,T.E., Brownstein,M.J., Uudin,T.B., Toshiyuki,S
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Pei
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibb
 Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Green,E.
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Shevchen
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,
 Butterfield,V.S., Krzywinaki,M.I., Skalska,U., Smailus
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 fu
 human and mouse cDNA sequences
 TITLE

11	PheIleValPhe-----PheTyrLeuTrp-----GlyLe	QY
	::	
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23	AlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValIle	QY
128	ACGGTTCTGAGCGGAGCTCTGATTCCTGAGCCAGAGTCAAAATCGAAGTTCT	Db
43	ProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr	QY
188	CCATTCAITCTGCATCGCAAGACCAAGGAGGGGATCTGATGTGTGCTCCACTA	Db
63	TyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGln	QY
248	TATTTAGAAAGGACGGCTCCCTGTTTCATTCCTCACTCACAAACATCAACATGG	Db
83	LysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaIle	QY
308	GTCTGTTTCACCTCGGCGATATCGAGAGTGTCTCAAAGGCTGGGACCAAGGCTT	Db
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368	ARGTGTGGGAGAGAGCGAAAGCTCCCGTTCCTTCCTCGCCCTGGGCTATGG	Db
123	GlyTyrAlaGluGlyLysIleProAspAlaThrLeuIlePheGluIleGln	QY
428	GGA-----AAAGGTAAATCCCTCCAGAGAGCACACTGATATTCAACATTGA	Db
143	AlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAs	QY
482	GAAATTCGAATGGCCCAAGTCCACGAGTGTGTTCAAGAAATGGACCTCAA	Db
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183	LysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys	QY
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Search completed: April 9, 2004, 11:57:53
Job time : 3769 secs

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through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
tigs: IRAK Plate: 23 Row: m Column: 1
; clone was selected for full length sequencing because it
used the following selection criteria: matched mRNA gi: 23956365.
Location/Qualifiers

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	10	Gaps:	4
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

aleic search, using frame_plus_p2n model

April 9, 2004, 08:38:41 ; Search time 416 Seconds
(without alignments)
2267.067 Million cell updates/sec

US-10-015-480A-180

1189
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 6747726

length: 0
length: 2000000000

: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

is the number of results predicted by chance to have a
ater than or equal to the score of the result being printed,
rived by analysis of the total score distribution.

SUMMARIES

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100.0	907	4 AAF54329	Aaf54329 DNA encod
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100.0	907	8 ACD68366	Acd68366 Novel hum
100.0	907	8 ACH04468	Ach04468 Human cDN
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31	1176	98.9	968	7	ADA40498	Ada40498
32	1176	98.9	968	8	ACH04906	Ach04906
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ALIGNMENTS

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AC AAA77672;
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DT 07-NOV-2000 (first entry)
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KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascular
diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hyp
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KW angioenic; proliferative; cardiant; cardiovascular; antiather
cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
XX
PN WO200032221-A2.
XX
XX
PD 08-JUN-2000.
XX
XX
PF 30-NOV-1999; 99WO-US028313.
XX
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.

9; 99US-0144758P.
9; 99US-0145698P.
9; 99WO-US020111.
9; 99WO-US020594.
9; 99WO-US020944.
9; 99WO-US021090.
9; 99WO-US021547.
9; 99WO-US023089.
9; 99US-0162506P.

NEMTECH INC.

AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
Watanabe CK, Williams PM, Wood WI;

-412154/35.
AB24429.

ids encoding PRO polypeptides useful for preventing, diagnosing
ing diagnosing a cardiovascular, endothelial or angiogenic
in mammals.

Fig 83; 315pp; English.

it invention describes nucleic acids encoding PRO polypeptides
; preventing, diagnosing and treating diagnosing a
ular, endothelial or angiogenic disorder in mammals by
cell proliferation, angiogenesis and cardiovascularisation,
identifying agonists and antagonists of these processes. The
ids and the proteins they encode may be used in the prevention,
and diagnosis of diseases associated with inappropriate PRO
such as cardiovascular, endothelial or angiogenic disorders in
g. atherosclerosis, cancers and cardiac hypertrophy). For
he nucleic acids (NCs) and vectors containing them and the PRO
he may be used to treat disorders associated with decreased PRO
1. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
and protein sequences used in the exemplification of the
vention

307 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

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1189.00 Matches: 222
city: 100.00% Conservative: 0
ilarity: 100.00% Mismatches: 0
100.00% Indels: 0
3 Gaps: 0

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GACGGCTACTGGCTAAAGACCGCTCGAAATTTCTACTGAGCGCGACACAAAATGAAGGC 262
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CACCCCAATAGTTGTTCTTGTGTGGCGAAGTCAATAAGGCGCTAGACATTGCTATG 322
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Db 323 ACAGATATGTGCGCTCGAGAAAGCGAAAGTAGTTATACCCCTTCATTG
Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
Db 383 AAGGAGGCTATGAGAGGAGGAGATTCCACCGATGCTACATTGATTTTG
Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
Db 443 CTTTATGCTGTGACCAAGGACCGAGCAGCATTGAGACATTTAAACAATAG
Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrIleuGlnArgGluP
Db 503 AATGACAGGCGAGCTCTCTAAAGCGGAGATAACCTCTACTTGCAGAGGAAT
Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
Db 563 GATGAGAGGCGACGTGACAGTCAATCATATCAGATGCAGTTTGTAGAGATATT
Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
Db 623 AATGACCATGATGCTGATGCTTCATTTCCTCCCAAGGATACATATGATACCI
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Db 683 GAACATA 688
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XX 08-AUG-2000 (first entry)
DT Human PRO1304 (UNQ670) cDNA sequence SEQ ID NO:179.
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KW transmembrane; secretion; immunoadhesion; pharmaceutical; scr
XX Homo sapiens.
XX WO200012708-A2.
XX 09-MAR-2000.
PF 01-SEP-1999; 99WO-US020111.
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
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PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
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PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
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 7 98US-0108500P.
 7 98US-0106464P.

PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
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 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
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 PR 17-NOV-1998; 98US-0108802P.
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 PR 17-NOV-1998; 98US-0108867P.
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 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood
 XX
 DR WPI; 2000-237871/20.
 DR P-PSDB; AAY99391.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or
 PT PRO polypeptides, useful for screening of potential peptide or
 PT molecule inhibitors of the relevant receptor/ligand interaction
 XX
 PS Claim 2; Fig 103; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembral
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY;
 CC transmembrane and receptor PRO proteins can be used for screen;
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide
 CC encoding then have various industrial applications, including
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 rep;
 CC primers and hybridisation probes used in the isolation of the
 CC polypeptides from the present invention
 XX
 SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.87e-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-015-480A-180 (1-222) x AAA37073 (1-907)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
 DB 23 ATGCCAAAACCATGCATTCTTATT CAGATTCAATGTTTCTTTTATCTGCG
 QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
 DB 83 TTTACTGCTCAGACAAAAGAAAGAGAGACACCGAAGAAGTCAAAATAGAT
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
 DB 143 CATCGTCCAGAAAACACTGCTCTAAGACAAAGCAAGGAGGAGACCTACTAAATGCG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsr

|||||ACGGCTACCTGGCTAAGACGGCTCGAAATTTCTACTGCGACCGGACACAAAATGAAGGC 262
 isProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 ACCCCAAATGGTGTGTCTGGGTGGGCAAGTCATATAAAGGCCCTAGACATTGCTATG 322
 hrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
 CAGATATGTCCTGGAGAAAGCGAAGTAGTTATACCCCTTCATTGTGATACGGA 382
 ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 AGAAGGCTATGCAGAAAGGCAGATTCCACCGGATGCTACATTGATTTTGGATTGAA 442
 euTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTTATGCTGTGACCAAGGACCGGAGCATTTGAGACATTTAAACAAATAGACATGGAC 502
 snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 ATGACAGGCGAGCTCTTAAGCCGAGATAAACCCTCTACTTGCAAGGGAATTTGAAAA 562
 spGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 ATGAGAAGCCACCGTACCAAGTCATATCAGGATGCAAGTTTGTAGAGATATTTTAAAGA 622
 snAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 ATGACCATGATGTGTGAGTGGCTTCATTCTCCCAAGGAATACAAATGATATACCAACGAT 682
 :luLeu 222
 :AACTA 688
 :standard; DNA; 907 BP.
 :1 (first entry)
 ng protein of the invention #52.
 transmembrane; gene therapy; ss.
 ed.
 :1-A1.
 :10.
 :10; 2000WO-US004342.
 :9; 99US-0141037P.
 :9; 99US-0144758P.
 :9; 99US-0145698P.
 :9; 99WO-US020111.
 :9; 99US-0182506P.
 :9; 99WO-US028313.
 :9; 99WO-US028551.
 :9; 99WO-US030095.
 :10; 2000WO-US000219.
 :10; 2000WO-US000376.
 :3NENTECH INC.
 Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 ddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 oni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 M, Wood WI;

DR WPI; 2001-071395/08.
 XX Secreted and transmembrane proteins and nucleic acids designat
 PT useful as hybridization probes, in chromosome and gene mapping
 PT therapy.
 XX Claim 2; Fig 103; 787pp; English.
 PS
 XX The present invention relates to secreted and transmembrane pr
 CC These proteins and the DNA encoding them may be used as hybrid
 CC probes, in chromosome and gene mapping and in the generation c
 CC sense RNA and DNA. They may also be used to generate eith
 CC transgenic animals or knockout animals which are in turn usefu
 CC development and screening of therapeutically useful reagents.
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.87e-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
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 DB 23 ATCCCAAAACCATGCAATTTCTATTTCAGATTCAATTTCTTTTATCTGTC
 QY 21 PheThrAlaGlnArgGlnLysLysGluLysThrGluGluValLysIleG
 DB 83 TTACTGCTCAGAGACAAAGAAAGAGAGAGAGACCCGAGAGCTGAAATAG
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
 DB 143 CATCGTCCAGAAAACCTCTTAAGACAAGCAAGCAAGAGGAGACCTACTAAATG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 DB 203 GACGGCTACCTGGCTAAGACGGCTCGAAATTTCTACTGACGCGGACACAA
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
 DB 263 CACCCCAATGGTGTCTTGTGTGGCAAGTCATATAAAGGCGCTAGACA
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 DB 323 ACAGATATGTGCTGAGAAAAGCGAAAAGTAGTTATATACCCCTTCATTTG
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 DB 383 AAGGAGGCTATGCAAGGCAAGATTCCACCGGATGCTACATTGATTTTGT
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
 DB 443 CTTTATGCTGTGACCAAGGACCCAGGACATTGAGACATTTAAACAAATAG
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
 DB 503 AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGAAGGAAT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
 DB 563 GATGAGAGGACGCTGCAAGTCATATCAGGATGCAAGTATTTAGAGATATTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
 DB 623 AATGACCATGATGTTGATGCTTCATTTCTCTCCNAGGAATACATGTATACCI
 QY 221 GluLeu 222

reted and transmembrane protein; PR0; angiogenesis;
l cell proliferation; wound healing; immune response;
tes proliferation; neonatal heart hypertrophy; tumour;
sufficiency disorder; calcium flux; inflammation;
endothelial growth factor-stimulated proliferation;
kidney mesangial cell proliferation; Berger disease;
V; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
herpetiformis; diabetes; haemoglobin switch; insulinaemia;
beta-cell precursor cell differentiation; thalassemias;
uditory hair cell regeneration; hearing loss; bone disorder;
disorder; sports injury; arthritis; gene; ss.

ns.

30-AL.

3.

1; 2001US-00015869.

8; 98US-0098716P.
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PR 21-OCT-1998; 98US-0105104P.
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PR 17-NOV-1998; 98US-0108801P.
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PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.

99US-0129674P.
99US-0141037P.
99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US021194.
99US-0162506P.
99WO-US028313.
99WO-US028551.
99WO-US030095.
2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004342.
2000WO-US005004.
2000WO-US005841.
2000WO-US006884.
2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
2000WO-US023522.
2000WO-US023328.
2000WO-US030952.
2000WO-US030873.
2000WO-US032678.
2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
dard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

85293/55.
33633.

ted PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
t modulate glucose or free fatty acid uptake by skeletal
s, and are useful for treating diabetes, hyper- or hypo-

2.87e-129 Length: 907
1189.00 Matches: 222
100.00% Conservatives: 0
100.00% Mismatches: 0
100.00% Indels: 0
8 Gaps: 0

80 (1-222) x ACD68366 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
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eThrAlaGlnArgGlnLysGluGluSerThrGluGluValLysIleGluValLeu 40
TACTGCTCAGACAAAAGAAAGAGGAGACCCGAGAGAGTGAATGAAATGAGTTTGG 142
sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TCGTCAGAAAATGCTCTAAGACAGCAAGAGAGGAGACCTACTTAATGCCATTAT 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCGCGCGACACAAATGAAGGC 262

QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
DDB 263 CACCCCAAAAGTTTGTCTTGGTGTGGCAAGTCATAAAGCGCTAGACATT
QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
DDB 323 ACAGATATGTCCTCGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTCG
QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGly
DDB 383 AAGGAGGCTATGCAAGAGGCAAGATTCCACCGATGCTCATTTGATTGAC
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
DDB 443 CTTTATGCTGTGACCAAGAGGACCGAGCATTCGAGCATTTAAACAAATAGAC
QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
DDB 503 AATGACAGGCGACTCTCTAAAGCGGAGATAACCTCTACTTGCAGGGAATT
QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
DDB 563 GATGAGAAGCCACGTCAGTCATATCAGGATGCGATTTTAGAAGATATTTT
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGly
DDB 623 AATGACCATGATGTTGATGGCTTCATTTCTCCAGGAGATACATGTATACCA
QY 221 GluLeu 222
DDB 683 GAACATA 688
RESULT 6
ACH04468
ID ACH04468 standard; cDNA; 907 BP.
AC ACH04468;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1304.
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis;
KW adrenal cortical capillary; endothelial cell growth; wound heal
KW stimulated T-lymphocyte proliferation; immune response suppress
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insu
KW chondrocyte redifferentiation; bone disorder; cartilage disorder
sports injury; arthritis.
Homo sapiens.
XX
PN US2003044841-A1.
XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
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PR 02-SEP-1998; 98US-0098803P.
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PR 17-NOV-1998; 98US-0108775P.
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PR 17-NOV-1998; 98US-0108867P.
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PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

2001US-00946374.

ENTECH INC.

Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S, Gdard A, Godowski Fu, Grimaldi JC, Gurney AL, Hillan KJ, ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI;

92259/46.

4486.

ted and transmembrane polypeptides and polynucleotides em useful for treating various cardiac insufficiency bone and/or cartilage disorders such as sports injuries and

2.87e-129 Length: 907
1189.00 Matches: 222
ty: 100.00% Conservative: 0
arity: 100.00% Mismatches: 0
100.00% Indels: 0
8 Gaps: 0

80 (1-222) x ACH04468 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPheTyrLeuTyrGlyLeu 20
GCGAAACATGCAATTTCTTATTCAGATTCATTTCTTTTATCTGGGGCCTT 82
eThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
TACTGCTCAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142
sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TCGTCCAGAAATGCTCTTAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAT 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGTACCTGGCTTAAGAGCGGCTCGAAATTTCTACGACCGGACACAAATGAAAGC 262
sProLysThrPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIleAlaMet 100
CCCCAAATGTTTCTTCTTGTGTGGCAAGTCATAAAGCGCTAGACATTGCTATG 322
rAspMetCysProGlyGluLysArgLysValValleProProSerPheAlaTyrGly 120
AGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCATACGGA 382
sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
GAGAGCTATGAGAAAGCAAGATTCACCGGATGCTACATTTATTTTGGATTGAA 442
uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTATGCTGTGACCAAGGACCGAGCATTGAGACATTTAAACAAATAGACATGGAC 502
nAspArgGlnLeuSerLysAlaGluLeuAsnLeuTyrLeuGlnArgGluPheGluLys 180
TGACAGGCGAGCTCTTAAAGCGGAGATAAACCTCTACTTGCAGAGGAAATTTGAAAA 562
pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
TGAGAGCCAGCTGACAGCTCATATCAGGATGCGAGTTTGTAGAGATATTTTAAAG 622
nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
TGACCATGATGTGTGGCTTCTTTCTCCAGGAGATACATGTATACCAACAGAT 682
uLeu 222
||||

683 GAACTA 688

RESULT 7

ACD68012

ID ACD68012 standard; cDNA; 907 BP.

XX AC ACD68012;

XX AC ACD68012;

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1304 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; v

KW

XX tissue typing; chromosome identification; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

FN US2003073129-A1.

XX

PD 17-APR-2003.

XX

PF 04-SEP-2001; 2001US-00946374.

XX

PR 01-SEP-1998; 98US-0098716P.

PR

PR 01-SEP-1998; 98US-0098723P.

PR

PR 01-SEP-1998; 98US-0098749P.

PR

PR 01-SEP-1998; 98US-0098750P.

PR

PR 02-SEP-1998; 98US-0098803P.

PR

PR 02-SEP-1998; 98US-0098821P.

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PR 02-SEP-1998; 98US-0098843P.

PR

PR 09-SEP-1998; 98US-0099536P.

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PR 09-SEP-1998; 98US-0099596P.

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PR 09-SEP-1998; 98US-0099598P.

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PR 09-SEP-1998; 98US-0099602P.

PR

PR 09-SEP-1998; 98US-0099642P.

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PR 10-SEP-1998; 98US-0099741P.

PR

PR 10-SEP-1998; 98US-0099754P.

PR

PR 10-SEP-1998; 98US-0099763P.

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PR 10-SEP-1998; 98US-0099792P.

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PR 10-SEP-1998; 98US-0099808P.

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PR 10-SEP-1998; 98US-0099812P.

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PR 10-SEP-1998; 98US-0099815P.

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PR 10-SEP-1998; 98US-0099816P.

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PR 15-SEP-1998; 98US-0100385P.

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PR 15-SEP-1998; 98US-0100388P.

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PR 15-SEP-1998; 98US-0100390P.

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PR 16-SEP-1998; 98US-0100584P.

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PR 16-SEP-1998; 98US-0100627P.

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PR 16-SEP-1998; 98US-0100683P.

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PR 17-SEP-1998; 98US-0100684P.

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PR 17-SEP-1998; 98US-0100710P.

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PR 17-SEP-1998; 98US-0100711P.

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PR 17-SEP-1998; 98US-0100919P.

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PR 17-SEP-1998; 98US-0100930P.

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PR 18-SEP-1998; 98US-0100848P.

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PR 18-SEP-1998; 98US-0101014P.

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PR 18-SEP-1998; 98US-0101068P.

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PR 18-SEP-1998; 98US-0101071P.

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PR 22-SEP-1998; 98US-0101279P.

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PR 23-SEP-1998; 98US-0101471P.

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PR 23-SEP-1998; 98US-0101472P.

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PR 23-SEP-1998; 98US-0101474P.

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PR 23-SEP-1998; 98US-0101475P.

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PR 23-SEP-1998; 98US-0101476P.

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PR 23-SEP-1998; 98US-0101477P.

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PR 23-SEP-1998; 98US-0101479P.

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PR 24-SEP-1998; 98US-0101738P.

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PR 24-SEP-1998; 98US-0101741P.

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PR 24-SEP-1998; 98US-0101743P.

PR

3; 98US-0101915P.
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 3; 98US-0108852P.
 3; 98US-0108858P.
 3; 98US-0108904P.

PR 22-DEC-1998; 98US-00218517.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 12-APR-1999; 99US-00284291.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 18-OCT-1999; 99US-00403297.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00882636.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WI;
 XX WPI; 2003-585292/55.
 DR P-P8DB; ABO33510.

XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, usef
 PT preparation of a medicament for treating a condition responsiv
 PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 2; Fig 103; 561pp; English.

XX The invention describes an isolated PRO (secreted and transmem
 CC polypeptide (1), having at least 80% sequence identity to a se

Alignment Scores:

Pred. No.:	2,87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-015-480A-180 (1-222) x ACD68012 (1-907)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr

DB 23 ATGCCAAAAACCATGCATTTCTATTCAGATTCATTTCTTTTATCTGTG

eThrAlaGlnArgGlnLysGluSerThrGluGluValLysIleGluValLeu 40
TACTGCTCAGACAAACAGAGAGAGAGACCGAAGAGTGAATAAGAGTTTG 142
SArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TGTTCAGAAAACCTGCTCTAAGACAAGCAAGAGGAGACCTACTATAATGCCCATTTAT 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGACCGCGGACACAAATGAAGGC 262
sProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100
CCCCAATGGTTTGTCTTGGTGTGGCAAGTCATAAAAGGCCATAGACATTGCTATG 322
rAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
AGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCTATACGGA 382
sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
GAGAGGCTATGAGAGGCAAGATCCACCGATGCTACATTGATTTTGAGATTGAA 442
uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTATGCTGTGACCAAGGACCGAGCATTCAGACATTTAAACAAATAGACATGCAC 502
nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
TGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGAAAA 562
pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
TGGAGAGCCACGTGACAGTCATATCAGGATGCGATTTTAGAGATATTTTAAGAG 622
nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
TGACCATGATGTGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACCAT 682

uLeu 222

ACTA 688

andard; cDNA; 907 BP.

(first entry)

olynucleotide #52.

gene; ss; protein electrophoresis; chromosome mapping;
g; genetic disorder.

s.

5-A1.

; 2001US-00013907.

; 98US-0098716P.

; 98US-0098723P.

; 98US-0098749P.

; 98US-0098750P.

; 98US-0098803P.

; 98US-0098821P.

; 98US-0098843P.

; 98US-0099536P.

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3: 98US-0105169P.
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 3: 98US-0114223P.
 9: 99WO-US000106.
 9: 99US-0129674P.
 9: 99US-0141037P.
 9: 99US-0144758P.
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 9: 99WO-US020111.
 9: 99WO-US021194.
 9: 99US-0162506P.
 9: 99WO-US028313.
 9: 99WO-US028551.
 9: 99WO-US030095.
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 0: 2000WO-US000376.
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 0: 2000WO-US005004.
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 0: 2000WO-US006884.
 0: 2000WO-US013705.
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 0: 2000WO-US015264.
 0: 2000WO-US023522.
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 0: 2000WO-US030873.
 0: 2000WO-US032678.
 1: 2001WO-US006520.
 1: 2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paori NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WI;
 XX WPI: 2003-555602/52.
 DR P-PSDB; ADC18049.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, usef
 PT preparation of a medicament for treating a condition responsiv
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX Claim 2; SEQ ID NO 179; 555pp; English.
 XX The invention relates to human PRO polypeptides and the polynu
 CC encoding them. The sequences are useful in the preparation of
 CC medicament for treating a condition responsive to a PRO polype
 CC polypeptides are useful in a number of functional biological a
 CC molecular weight markers for protein electrophoresis and as th

Alignment Scores:
 Pred. No.: 2,87e-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-015-480A-180 (1-222) x ADC18048 (1-907)

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 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGI
 Db 83 TTTACTGCTCAGACAAAAGAAAGAGGAGAGCACCAGAAAGAGTGAATAAGA
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl
 Db 143 CATCGTCCAGAAACTGCTTAAGACACAGCAAGAGGGAGACTACTAAATGC
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
 Db 203 GACGGCTACCTGGCTAAGACCGGCTCGAATTTCTACTGCGCGGACACAAA
 QY 81 HisProLysTyrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl
 Db 263 CACCCCAAAATGTTTCTTGTGTGGCAAGTCAATAAAGAGCGCTAGACAT
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTGTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGI
 Db 383 AAGGAGGCTATGCAGAGGCAAGATTCCACCGGATGCTACATTGATTTTGN
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGGACCCAGGAGCATTTAGACATTTAAACAAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 AATGACAGGCAGCTCTCTTAAGCCGAGATAAACCTCTACTTGCAGAGGGAATT

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 TGACCATGATGGTGGTGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT 682

uLeu 222

|||||
 ACTA 688

andard; cDNA; 907 BP.

(first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
 onset; cardiac insufficiency disorder; calcium flux;
 ein endothelial cell; bone disorder; cartilage disorder;
 wound healing; diabetes; skeletal muscle cells; obesity;
 ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 herpeticiformis; Crohn's disease; thalassaemia.

S.

5-A1.

; 2001US-00015386.

98US-0098716P.
 98US-0098723P.
 98US-0098749P.
 98US-0098750P.
 98US-0098803P.
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Matches: 222

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Qy	21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGln		
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Qy	61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs		
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XX	AC	ADD39771;	
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XX	DE	Human cDNA encoding secreted/transmembrane protein PRO1304.	
XX	KW	Human; ss; gene; secreted protein; transmembrane protein; PRO;	
XX	KW	immune response; cardiac insufficiency disorder; calcium flux;	
XX	KW	umbilical vein endothelial cell; bone disorder; cartilage diso;	
XX	KW	arthritis; wound healing; diabetes; skeletal muscle cells; obe	
XX	KW	Berger disease; nephropathy; Schönlein-Henoch purpura; coelic	
XX	KW	dermatitis; herpeticformis; Crohn's disease; thalassemia.	
XX	OS	Homo sapiens.	

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99WO-US028313.
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2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Girdard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Ni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI;

55122/71.
39772.

d and transmembrane PRO polypeptides useful for treating dney disorders, Crohn's disease, diabetes mellitus, hyper- or nemia, sports injuries and arthritis.

Q ID NO 179; 557pp; English.

on relates to an isolated PRO polypeptide (secreted or ne protein) having at least 80% amino acid sequence identity acid sequence chosen from 123 fully defined sequences as e specification (including their extracellular domains either their associated signal peptides. Also include are the (NA) sequences encoding PRO, a vector comprising the PRO NA, a omprising the vector, producing PRO, a chimaeric molecule PRO fused to a heterologous amino acid sequence, and an anti-y. PRO is useful as molecular weight markers for protein esis and also for chromosome identification. PRO is also tissue typing. PRO and PRO NA are useful as hybridisation a CDNA library to isolate the full-length PRO CDNA. PRO NA is generating transgenic animals or knock-out animals which are evelopment and screening useful reagents. PRO NA is also ene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are treating cancerous tumours. PRO1250, PRO1418 and PRO1410 s are useful for suppressing immune response. PRO1246 is useful for treating cardiac insufficiency disorders. ypeptide is also useful for treating tumours. PRO1246 and ypeptide are useful for stimulating calcium flux in human

CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474 CC polypeptides are useful for treating bone and/or cartilage disc CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1 CC polypeptides are useful for treating diabetes in skeletal musc CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are usef CC treating Berger disease or other nephropathies associated with CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or (CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, CC PRO1410 and PRO1575 are useful in treating thalassaemias. The i CC sequence encodes a PRO protein of the invention.

XX
SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-10-015-480A-180 (1-222) x ADD39771 (1-907)

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QY	21	PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
DB	83	TTTACTGCTCAGACACAAAAGAAAGAGAGAGACCCGGAAGAGTGAATAGAT
QY	41	HisArgProGluAenCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
DB	143	CATCGTCCAGAAAACACTGCTCTAAGACAAAGCAAGAGGAGACCTACTAAATGTC
QY	61	AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsi
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QY	81	HisProLysThrPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIle
DB	263	CACCCCAAAATGTTTGTCTTGTGGTGGCAAGTATATAAAGGCGCTAGACAT
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QY	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
DB	383	AAGGAGGCTATGCAGAAAGCAAGATTCACCGGATGCTACATTGATTTTGA
QY	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
DB	443	CTTTATGTGTGACCAAAAGGACCCAGGAGCATTTAGACATTTAAACAAATAGA
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DB	503	AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGAATTT
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standard; cDNA; 907 BP.

1 (first entry)

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ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
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36-Al.

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2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Deanovers L, Eaton DL, Ferrara N, Fong S;
dard A, Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ;
ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

08344/67.
70218.

ted PRO polypeptide useful for tissue typing, modulating
activity of cell, as molecular weight markers in protein
esis, for treating arthritis, tumor.

Q ID NO 179; 549pp; English.

on relates to an isolated PRO polypeptide (secreted or

2.87e-129 Length: 907
1189.00 Matches: 222
ty: 100.00% Conservative: 0
arity: 100.00% Mismatches: 0
Indels: 0
9 Gaps: 0

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Db 203 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACCGGACACAAAA
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QY 101 ThrAspMetCysProGlyGluLysArgLysValValLysProProSerPheAla;
Db 323 ACAGATATGTCCTGGAGAAAGCGAAAGCTAGTATTACCCCTTCATTGGC
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QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
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QY 221 GluLeu 222
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AC ADD38338;
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DT 15-JAN-2004 (first entry)
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KW Human; s8; gene; secreted protein; transmembrane protein; PRO;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disor
KW arthritis; wound healing; diabetes; skeletal muscle cells; obes
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
OS Homo sapiens.
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PD 22-MAY-2003.
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eThrAlaGlnArgGlnIleValysGluGluSerThrGluGluValIleGluValLeu 40
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 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F.
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, W
 PI Williams FM, Wood W;

XX WPI; 2003-786999/74.
 DR P-PSDB; ADD39295.

PT Novel isolated PRO polypeptide useful for tissue typing, modul
 PT biological activity of cell, as molecular weight markers in pr
 PT electrophoresis, for treating arthritis, tumor.

XX Claim 2; SEQ ID NO 179; 550pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted

Alignment Scores:

Pred. No.:	2.87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	10-NOV-2000;	2000WO-US030873.	
PR	01-DEC-2000;	2000WO-US032678.	
PR	28-FEB-2001;	2001WO-US006520.	
PR	01-MAR-2001;	2001WO-US006666.	
PR	01-JUN-2001;	2001WO-US017800.	
PR	20-JUN-2001;	2001WO-US019692.	
PR	29-JUN-2001;	2001WO-US021066.	
PR	09-JUL-2001;	2001WO-US021735.	
PR	04-SEP-2001;	2001US-00946374.	
XX			
XX	(GETH) GENENTECH INC.		
XX			
PI	Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, F		
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H		
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W		
PI	Williams PM, Wood WI;		
XX			
DR	WPI; 2003-765477/72.		
DR	P-PSDB; ADD38818.		
XX			
PT	New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018,		
PT	PRO1244, PRO1246, useful for treating cancerous tumors, cardia		
PT	insufficiency disorders, wound healing, Crohn's disease, celia		
XX			
PS	Claim 2; SEQ ID NO 179; 555pp; English.		
XX			
CC	The invention relates to an isolated PRO polypeptide (secreted		
Alignment Scores:			
Pred. No.:	2,87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0
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Qy	1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTi		
Db	23 ATGCCAAAACCATGCATTTCTTATTTCAGATTCATTTCTTTTATCTGTC		
Qy	21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG		
Db	83 TTTACTTGCTCAGAGACAAAAGAAGAGAGAGAGACCGAAGAGTGAATAATG		
Qy	41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl		
Db	143 CATCGTCCAGAAATCTCTTAAGACAGACCAAGAGGAGACCTACTAAATGC		
Qy	61 AspGlyTyrIleuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs		
Db	203 GACGGGTACTCGCTAAAGACGGCTCGAAATTTCTACTGCACGGGACACAAAF		
Qy	81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl		
Db	263 CACCCCAATATGGTTTGTCTTGTGTGTGGCAAGTCAATAAAGCCCTAGACAI		
Qy	101 ThrAspMetCysProGlyGluLysArgLysValIleProProSerPheAl		
Db	323 ACAGATATGTCCTCGAGAAAGCGAARAAGTAGTTATACCCCTTCATTTC		
Qy	121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeullePheGl		
Db	383 AAGGAAGGCTATGCAGAAGCAAGATTTCCACCGGATGCTACATTGATTTTGTG		

uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
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 pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 TGAAGACCCAGTCGACAGTCATATCAGGATGCGAGTTTGAAGATATTTTAAGAG 622
 nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 TGACCATGATGTGTGATGGCTTCATTTCTCCCAAGGAATACATGTATATACCAACAGAT 682

uLeu 222

ACTA 688

andard; cDNA; 907 bp.
 (first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
 onse; cardiac insufficiency disorder; calcium flux;
 ein endothelial cell; bone disorder; cartilage disorder;
 wound healing; diabetes; skeletal muscle cells; obesity;
 ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 herpeticiformis; Cronh's disease; thalassaemia.

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; 2001US-00006117.

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1	2001WO-US019632
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1	2001WO-US021735
1	2001US-00946374

VENTECH INC.

Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S, Iddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Ioni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK, Wu M, Wood WI;

755104/71.
D40249.

ed PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773, RO1246, are useful for treating cancerous tumors and cardiac ncV disorders.

PS	Claim 2; SEQ ID NO 179; 550pp; English.	
XX		
XX		
CC	The invention relates to an isolated PRO polypeptide (secreted	
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US-10-015-480A-180 (1-222) X ADD40248 (1-907)

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us-10-015-480a-180.rnpb

GenCore version 5.1.6
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April 9, 2004, 10:47:52 ; Search time 2260 Seconds
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368.506 Million cell updates/sec

US-10-015-480a-180

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Fgapop 6.0 , Fgapext 7.0

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Maximum Match 100%

Listing first 45 summaries

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ived by analysis of the total score distribution.

SUMMARIES

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Query Match Length DB ID Description

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ALIGNMENTS

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; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurrey, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

Williams, P. Mickey
Wood, William I.
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 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C14
 ; CURRENT APPLICATION NUMBER: US/10/006.856A
 ; CURRENT FILING DATE: 2002-05-10
 ; NUMBER OF SEQ ID NOS: 477
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 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
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 Query Match: 100.00% Indels: 0
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aker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Paul J.
Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth J.

PAHLI, Nicholas F.
 ENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ENTION: Acids Encoding the Same
 CE: P2830P1C4
 ICATION NUMBER: US/10/006,818A
 NG DATE: 2001-12-06
 ation removed - See File Wrapper or Palm
 O ID NOS: 477

omo sapiens
179

s:	9.97e-148	length:	907
	1189.00	Matches:	222
ity:	100.00%	Conservative:	0
arity:	100.00%	Mismatches:	0
	100.00%	Indels:	0

DB:	14	Gaps:	0
US-10-015-480A-180 (1-222) x US-10-006-818A-179 (1-907)			
QY	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuT	
Db	23	ATGCCAAAACCCANGCATTTCTATTACAGATTCAATGTTTCTTTTATCTGTC	
QY	21	PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG	
Db	83	TTTACTGCTCAGAGACAAAGAAAGAGGAGCACCGAAGAGTGAATAAGT	
QY	41	HisArgProGluIleuLysSerLysThrSerLysLysGlyAspLeuLeuAsnAl	
Db	143	CATCGTCCAGAAATGCTCTAAGACAAAGCAAGAGGAGACCTTACTAAATGC	
QY	61	AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs	
Db	203	GACGGCTACTCGCTAAAGACGGCTCGAAATTTCTACTGCGCCGGACACAAAF	
QY	81	HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl	
Db	263	CACCCCAATGGTTTGTCTTGTGTGTGGCGAGTCATAAAGGCCCTAGACAT	
QY	101	ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl	
Db	323	ACAGATATGTCCTCGAGAAAAGCGAAAAAGTAGTTATACCCCTTCATTTGCG	
QY	121	LysGluGlyTyrAlaGluGluLysIleProProAspAlaThrIleuIlePheGl	
Db	383	AAGGAAGGCTATCGAAGAGCAGATTCCACCGATGCTCACTTGTATTTTTF	
QY	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs	
Db	443	CTTTATGCTGTGACCAAGAGCACCGAGGCAATTGAGCATTTAAACAATAAGT	
QY	161	AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP	
Db	503	AATGACGGCAGCTCTTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAAT	
QY	181	AspGluIlyProArgaspLysSerTyrGlnAspAlaValLeuGluAspIleP	
Db	563	GATGAGAAGCCCGTGACAAAGTCAATCATCAGATGTCAGTTTTAGGAAGATATT	
QY	201	AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrIleValTyrGl	
Db	623	AATGACATGATGATGTCCTTCATTTCTCCCAAGGAATACATGATATACCP	
QY	221	Glueu 222	
Db	683	GAACCTA 688	

RESULT 4

RESUL* 4
US-10-015-393A-179
; Sequence 179, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferriara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
; TITLE OF INVENTION: Acids Encoding the Same

TE: P2830PIC46
 CATION NUMBER: US/10/015,393A
 IG DATE: 2002-06-10
 tion removed - See File Wrapper or Palm
 ID NOS: 477

mo sapiens
 79

9.97e-148 Length: 907
 1189.00 Matches: 222
 ty: 100.00% Conservative: 0
 arity: 100.00% Mismatches: 0
 Indels: 0
 Gaps: 14

.80 (1-222) x US-10-015-393A-179 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 GCCAAAACCATGCAATTCCTTATTCAGATTCATGTTCTTTTATCTGCGGCGCTT 82
 eThrAlaGlnArgGlnLysGluGluSerThrGluGluValLysIleGluValLeu 40
 TACTGTCTCAGAGCAAAAAGAGAGGAGAGCAGCCGAGAAAGTGAATAATAGAGTTTG 142
 sArgProGluAspCysSerLysThrSerLysGlyAspLeuLeuAsnAlaHisTyr 60
 TCGTCCAGAAAACCTGCTTAAGACAGCAAGAGAGGAGACCTACTAAATGCCCATAT 202
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 CGGCTACCTGGCTAAAGAGCGCTCGAAATCTACTGCGCGGACACAAATAGAGGC 262
 sProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 ACCCAAAATGTTTGTCTTGTGTTGGCAAGTCATAAAGGCGCTAGACATTCGTATG 322
 rAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
 TAGATATGTGCGCTCGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTTCATACGGA 382
 sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 GGAAGCTATGCAGAGGCGAAGATTCACCGGATGCTACATTCATTTTTCAGATTGAA 442
 uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTATGCTGTGACCAAGGACCCAGGAGCAATGAGACATTTAAACAAATAGACATGGAC 502
 nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 TGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTACTTCGAAAGGAAATTCAGAAA 562
 pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 TGAGAGCCACGTGACAGATCATATCAGGATGCGATTTTGAAGATATTTTGAAGAG 622
 nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 VTGACCATGATGGTGTGCTTCTCTCCAGGAATACATGTATATACCAACACCAT 682
 uLeu 222
 ACTA 688

79
 Application US/10015869A
 US20030073130A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Forg, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830PIC45
 CURRENT APPLICATION NUMBER: US/10/015,869A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 179
 LENGTH: 907
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-015-869A-179

Alignment Scores:
 Pred. No.: 9.97e-148 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 US-10-015-480A-180 (1-222) x US-10-015-869A-179 (1-907)

Qy 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrp
 Db 23 ATGCCAAAACCATGCAATTCCTTATTCAGATTCATGTTCTTTTATCTGTTG
 Qy 21 PheThrAlaGlnArgGlnLysGluGluSerThrGluGluValLysIleGlu
 Db 83 TTTACTGTCTCAGAGCAAAAAGAGAGGAGAGCAGCCGAGAAAGTGAATAATAG
 Qy 41 HisArgProGluAsnCysSerLysThrSerLysGlyAspLeuLeuAsnAla
 Db 143 CATGCTCCAGAAAACCTGCTCTAAGACAAAGCAAGAGGAGGACCTACTAAATGCG
 Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsi
 Db 203 GACGGCTACCTGGCTTAAGACGGCTCGAAATTCCTACTGCGCGGAGACAAAA
 Qy 81 HisProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
 Db 263 CACCCCAAAATGTTTGTCTTGTGTTGGCAAGTCATAAAGGCGCTAGACAT
 Qy 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
 Db 323 ACAGATATGTCCTCGGAGAAAAGGAAAAGTAGTTATACCCCTTCATTTGCG
 Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
 Db 383 AAGGAAGGCTATGCAAGAGCAAGATCCACCGGATGCTACATTCATTTTGA
 Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
 Db 443 CTTTATGCTGTGACCAAGAGGACCCAGGAGCATTCGAGACATTTAAACAAATAG
 Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
 Db 503 AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGTCAAAGGGAATTT

spGluysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLeuLys 200
 ATGAGAAGCCACGTCACAGTCAATATCAGATGCAGTATTTTAAAGATATTTTAAAG 622
 sNAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 ATGACCATGATGGTATGGCTTCATTCTCCCAAGGAATACAAATGATATACCAACGAT 682
 lueu 222
 |||||
 AACTA 688

179
 Application US/10012121A
 O. US20030073810A1
 MARION:
 Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan I.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 ENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ENTION: Acids Encoding the Same
 CE: P2830P1C20
 ICATION NUMBER: US/10/012.121A
 NG DATE: 2001-12-07
 ation removed - See File Wrapper or Palm
 Q ID NOS: 477

omo sapiens
 179

S: 9.97e-148 Length: 907
 1189.00 Matches: 222
 ity: 100.00% Conservative: 0
 larity: 100.00% Mismatches: 0
 100.00% Indels: 0
 14 Gaps: 0

180 (1-222) x US-10-012-121A-179 (1-907)

etProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 TGCCAAAACCAACGATTCCTTATTCAGATTCATTGTTTCTTTATCTGCGGGCCTT 82
 heThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
 TTACTGCTCAGACACAAAAGAAAGAGAGAGACCCGAGAAAGTGAATAATAGAGTTTGT 142
 tisArgProGluAnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 ATCGTCAGAAAACCTGCTCTTAAGACAGCAAGAGGAGACCTACTATAATGCCCCATAT 202
 aspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 AACGGCTACCTGGTAAAGACGGCTCGAAATCTACTGCGAGCCGAGACACAAATGAAGGC 262
 tisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100

Db 263 CACCCCAATGGTTTGTCTTGTGTGGCAAGTCATAAAAGGCCTAGACAI
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCCCTCGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGl
 Db 383 AAGGAAGGCTATGCAGACAGCAAGATTCCACCGGATGTACATTGATTTTGA
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGAGCACCGAGCATTTAGACATTTTAAACAAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 ATGCAGAGCAGCTCTCTTAAGCCGAGATAAACCTCTACTTGCAGAGATATT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCACGTCACAGTCATATCAGGATGCAGTTTATAGAGATATTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGl
 Db 623 AATGACCATGATGGTATGGCTTCATTCTCCCAAGGAATACAAATGATATACCA
 QY 221 Glueu 222
 |||||
 Db 683 GAACTA 688

RESULT 7
 US-10-006-116A-179
 : Sequence 179, Application US/10006116A
 : Publication No. US20030082626A1
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan I.
 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, Christopher J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 : TITLE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2830P1C15
 : CURRENT APPLICATION NUMBER: US/10/006,116A
 : CURRENT FILING DATE: 2001-12-16
 : PRIOR APPLICATION NUMBER: 60/098716
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098723
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098749
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098750
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098803
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/098821
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/098843
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/099536
 : PRIOR FILING DATE: 1998-09-09
 : PRIOR APPLICATION NUMBER: 60/099596
 : PRIOR FILING DATE: 1998-09-09
 : PRIOR APPLICATION NUMBER: 60/099598

us-10-015-480a-180.rnpb

1	PRIOR APPLICATION NUMBER: 60/101479
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/101738
4	PRIOR FILING DATE: 1998-09-24
5	PRIOR APPLICATION NUMBER: 60/101741
6	PRIOR FILING DATE: 1998-09-24
7	PRIOR APPLICATION NUMBER: 60/101743
8	PRIOR FILING DATE: 1998-09-24
9	PRIOR APPLICATION NUMBER: 60/101915
10	PRIOR FILING DATE: 1998-09-24
11	PRIOR APPLICATION NUMBER: 60/101916
12	PRIOR FILING DATE: 1998-09-24
13	PRIOR APPLICATION NUMBER: 60/102207
14	PRIOR FILING DATE: 1998-09-29
15	PRIOR APPLICATION NUMBER: 60/102240
16	PRIOR FILING DATE: 1998-09-29
17	PRIOR APPLICATION NUMBER: 60/102307
18	PRIOR FILING DATE: 1998-09-29
19	PRIOR APPLICATION NUMBER: 60/102330
20	PRIOR FILING DATE: 1998-09-29
21	PRIOR APPLICATION NUMBER: 60/102331
22	PRIOR FILING DATE: 1998-09-29
23	PRIOR APPLICATION NUMBER: 60/102484
24	PRIOR FILING DATE: 1998-09-30
25	PRIOR APPLICATION NUMBER: 60/102487
26	PRIOR FILING DATE: 1998-09-30
27	PRIOR APPLICATION NUMBER: 60/102570
28	PRIOR FILING DATE: 1998-09-30
29	PRIOR APPLICATION NUMBER: 60/102571
30	PRIOR FILING DATE: 1998-09-30
31	PRIOR APPLICATION NUMBER: 60/102684
32	PRIOR FILING DATE: 1998-10-01
33	PRIOR APPLICATION NUMBER: 60/102687
34	PRIOR FILING DATE: 1998-10-01
35	PRIOR APPLICATION NUMBER: 60/102965
36	PRIOR FILING DATE: 1998-10-02
37	PRIOR APPLICATION NUMBER: 60/103258
38	PRIOR FILING DATE: 1998-10-06
39	PRIOR APPLICATION NUMBER: 60/103314
40	PRIOR FILING DATE: 1998-10-07
41	PRIOR APPLICATION NUMBER: 60/103315
42	PRIOR FILING DATE: 1998-10-07
43	PRIOR APPLICATION NUMBER: 60/103328
44	PRIOR FILING DATE: 1998-10-07
45	PRIOR APPLICATION NUMBER: 60/103395
46	PRIOR FILING DATE: 1998-10-07
47	PRIOR APPLICATION NUMBER: 60/103396
48	PRIOR FILING DATE: 1998-10-07
49	PRIOR APPLICATION NUMBER: 60/103401
50	PRIOR FILING DATE: 1998-10-07
51	PRIOR APPLICATION NUMBER: 60/103449
52	PRIOR FILING DATE: 1998-10-06
53	PRIOR APPLICATION NUMBER: 60/103633
54	PRIOR FILING DATE: 1998-10-08
55	PRIOR APPLICATION NUMBER: 60/103678
56	PRIOR FILING DATE: 1998-10-08
57	PRIOR APPLICATION NUMBER: 60/103679
58	PRIOR FILING DATE: 1998-10-08
59	PRIOR APPLICATION NUMBER: 60/103711
60	PRIOR FILING DATE: 1998-10-08
61	PRIOR APPLICATION NUMBER: 60/104257
62	PRIOR FILING DATE: 1998-10-14
63	PRIOR APPLICATION NUMBER: 60/104987
64	PRIOR FILING DATE: 1998-10-20
65	PRIOR APPLICATION NUMBER: 60/105000
66	PRIOR FILING DATE: 1998-10-20
67	PRIOR APPLICATION NUMBER: 60/105002
68	PRIOR FILING DATE: 1998-10-20
69	PRIOR APPLICATION NUMBER: 60/105104
70	PRIOR FILING DATE: 1998-10-21
71	PRIOR APPLICATION NUMBER: 60/105169
72	PRIOR FILING DATE: 1998-10-22
73	PRIOR APPLICATION NUMBER: 60/105266

DATE: 1998-10-22
 ATION NUMBER: 60/105693
 DATE: 1998-10-26
 ATION NUMBER: 60/105694
 DATE: 1998-10-26
 ATION NUMBER: 60/105807
 DATE: 1998-10-27
 ATION NUMBER: 60/105881
 DATE: 1998-10-27
 ATION NUMBER: 60/105882
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

3: 9.97e-148 Length: 907
 1189.00 Matches: 222
 Conservative: 0
 Identity: 100.00% Mismatches: 0
 Indels: 0
 Gaps: 14

180 (1-222) x US-10-006-116A-179 (3-907)

atProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 TSCCAAAAACCATGCTATCTTATTCAGATTCATTGTTTCTTTTATCTGTGGGCGCTT 82
 aeThrAlaGlnArgGlnLysLysGluSerThrGluValLysLysLeuValLeu 40
 TTACTGCTCAGAGACAAAG 142
 isArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuAsnAlaHisTyr 60
 ATGCTCCAGAAAACCTGCTCTAGACACAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 202
 spGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGly 80
 ACGGCTACCTGGCTAAAGACGCTCGAATCTCTAGCAGCGGACACAAATGAAGGC 262
 isProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIleAlaMet 100
 ACCCAAAATGGTTGTTCTTGTGTTGGGCAAGTCTAAAGAGCGCTAGACATTGCTATG 322
 hrAspMetCysProGlyGluLysArgGlyValValLysPheAlaTyrGly 120
 CAGATATGTGCTGAG 382
 ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIleGlu 140
 AGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATTGATTTTGAATTTGAA 442
 euTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTTATGCTGTGACCAAGAGACACCGAGCATTTAGACATTTTAAACAAATAGACATGG 502
 snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 ATGACAGGCGCTCTCTAAGCGGAGATTAACCTCTACTTGCAGAGGAGATTGAAAAA 562
 spGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLys 200
 ATGAGAAGCCACGTCAGCAAGTCATATCAGGATGCGATTTTGAAGATTTTAAAGAG 622
 snAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 ATGACCATGATGGTGCTTCATTTCTCCCAAGGAATACAAATGTATATACCAACGAT 682
 luLeu 222
 AACTA 688

US-10-006-117A-179
 ; Sequence 179, Application US/100061117A
 ; Publication No. US20030082627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; FILE REFERENCE: P2830P1C13
 ; CURRENT APPLICATION NUMBER: US/10/006,117A
 ; Prior Filing DATE: 2002-03-19
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-006-117A-179

Alignment Scores:
 Pred. No.: 9.97e-148 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-006-117A-179 (1-907)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
 Db 23 ATGCCAAAACCATGCTATCTTATTCAGATTCATTGTTTCTTTTATCTGTG
 QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleG
 Db 83 TTTACTGCTCAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuAsnAl
 Db 143 CATGCTCCAGAAAACCTGCTCTAAGACACAGAGAGAGAGAGAGAGAGAGAG 60
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
 Db 203 GACGGCTACCTGGCTAAAGACGCTCGAATTTCTACTGCGCGGACACAAAA 60
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspIle
 Db 263 CACCCCAAAATGGTTTCTTGTGTTGGGCAAGTCATAAAAGGCGCTAGACAT 60
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 Db 383 AAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATTGATTTTGA 60
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60

nAspArgGlnLeuSerIysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 .TGACAGGACGCTCTAAAGCCGAGATAAACCTCTACTTGCNAAAGGAATTTCAGAAA 562
 pGluLysProArgAspIysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 .TGAGAAGCCACGTCGACAAAGTCATATCAGGATGCAGTTCATAGAAATATTTTAAAGA 622
 nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisasp 220
 .TGACCAATGATGGTGGCTTCATTTCTCCCAAGGAATACAATGTATACACACGAT 682

uLeu 222
 ACTA 688

79 Application US/10017527A
 . US20030082628A1
 ATION:

ker, Kevin P.
 oststein, David
 esnoyers, Luc
 aton, Dan I.
 errara, Napoleone
 ong, Sherman
 ao, Wei-qiang
 oddard, Audrey
 odowski, Paul J.
 rimaldi, Christopher J.
 urney, Austin L.
 illan, Kenneth J.
 an, James

anoni, Nicholas F.
 NTION: Secreted and Transmembrane Polypeptides and Nucleic
 NTION: Acids Encoding the Same

E: P2830PlC63
 CATION NUMBER: US/10/017,527A

G DATE: 2001-12-13

TION NUMBER: 60/098716
 DATE: 1998-09-01
 TION NUMBER: 60/098723
 DATE: 1998-09-01
 TION NUMBER: 60/098749
 DATE: 1998-09-01
 TION NUMBER: 60/098750
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 ; PRIOR APPLICATION NUMBER: 60/102207

Alignment Scores:			
Pred. No.:	9.97e-148	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0
US-10-015-480A-18C (1-222) x US-10-017-527A-179 (1-907)			
Qy	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr	
Db	23	ATGCCAAAACCATGCATTTCTTATTCAGATTCAATGTGTTTCTTTTATCTGTGG	
Qy	21	PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGl	
Db	83	TTTACTGCTCAGAGACAAAAGAAAGAGAGACCGAAGAGTGAATAATAGP	
Qy	41	HisArgProGluLanCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl	
Db	143	CATCGTCCGAAAACCTGCTCTTAAGACAAGCAGAAAGGAGACCTACTAAATGTC	
Qy	61	AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs	
Db	203	GACGGCTACCTGGCTAAAGCGGCTCGAATCTTACTGCAGCCCGACACAAA	
Qy	81	HisProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIl	
Db	263	CACCCCAATGGTTTGTCTTGTGTGGCAAGTCATAAAAGGCGCTAGACAT	
Qy	101	ThrAspMetCysProGlyGluLysArgLysValLlleProProSerPheAl	
Db	323	ACAGATATGTCCTCGAGAAAACGAAAAAGTAGTTATPACCCCTTCAITTTG	
Qy	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGl	
Db	383	AAGGAAGGCTATGCAGAAAGCAAGATTCCACCGATGCTACATTGATTTTTG	
Qy	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs	
Db	443	CTTTATGCTGTGACAAAGACCAACGAGCATTCAGACATTTAAACACAAATAGP	
Qy	161	AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPt	
Db	503	AATGACAGGACAGCTCTCTTAAGCCGAGATAAAGCTCTACTTTGCAAGAGGAAT	
Qy	181	AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh	
Db	563	GATGAGAAGCCACGTCGACAAAGTCATATCAGGATGCAGTGTTTTGAAGATATTTT	
Qy	201	AsnAspHisAspGlyAspGlyPheIleSerProLysGlnTyrAsnValTyrGl	
Db	623	AATGACCATGATGTGTAGTGCTTCATTTCTCCCAAGGAATACAATGTATACCA	
Qy	221	GluLeu 222	
Db	683	GAACATA 688	
RESULT 10			
US-10-013-913A-179			
; Sequence 179, Application US/10013913A			
; Publication No. US20030083462A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan I.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			

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Primaldi, Christopher J.
Burney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
REMARK: Secreted and Transmembrane Polypeptides and Nucleic
REMARK: Acids Encoding the Same
ID: F2830F1C40
CATION NUMBER: US/10/013,913A
IG DATE: 2002-07-15
ation removed - See File Wrapper or PalM
} ID NOS: 477

xmo sapiens
.79

3:      9.97e-148      Length:      907
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      100.00%      Conservative: 0
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80 (1-222) x US-10-013-913A-179 (1-907)

t:ProLysThrMetHisPheLeuPheAtqPheIleValPhePheTyrLeuTrpGlyLeu 20
GCCAAAAACCATGCATTTCATTTCAGATTTCATTGTTTCCTTTATCTGTGGGCCCT 40
e:ThAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
TACTGTCTCAGAGACAAAGAAGAGGAGGAGACCGACGAGCACTGAAATAGAGTTTG 142
s:ArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TCTGTCACAAAACCTCTCTAAGACAAGCAAGCAAGGAGGACCTACTAAATGCCATTAT 202
pGlyTyrIleuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGCGTCACTCGCTAAGACGCTCGAAATCTCTCTGCAGCCGCGACACAAATGAAGC 262

sProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
.CCCCAAAATGGTTGTTCTTGTTGTTGTCGCAACTCATAAAGCCCTGACATTGCTATG 322

rAspMetCysProGlyGluLysArgLysValValIleProSerPheAlaTyrGly 120
AGATATGTGCCCTCGAGAAAAGCGAAAGTAGTTATATACCCCTTCATTTGCATACGA 382

sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
GGAAGGCTATGCAAGACCAAGATTCCACCGGATGCTACATTGATTTTTCAGATTGAA 442

uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTATGCTGTGACCAAGACCAACGAGCATTTGAGACATTTAAACAAATAGACATPGAC 502

mAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
TGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTCGAAAGGGAATTTGAAANA 562

pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
TGAGAAGCCACGTCACAAAGTCATATCAGGATGCAAGTTTGAAGATATTTTAAAGAG 622

mAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
TGACCATGATGGTGAATGCTTCATTTCTCCCAAGGAATACAATGATATACCAACACGAT 682

uLeu 222

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Query Match:	100.00%	Indels:	0
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US-10-015-480a-180 (1-222) x US-10-007-194A-179 (1-907)

Qy	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
Db	23	ATGCCAAACCAACGATTCATTATTCAGATTCATTTCTTTTATCTGIG

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leThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysLysLeuValLeu 40
|||||
TACTGCTCAGACACAAAGAAAGAGGAGAGCACCAGAGAGTGAATATAGATTTC 142
|||||
.sArgProGluAAsnCysSerLysThrSerLysLysGlyAspLeuAsnAlaHisTyr 60
|||||
TCTGCTCCAGAAAACCTGCTTAAGACAGCAAGAGGAGAGCTACTAAATGCCATTAT 202
|||||
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
|||||
ACGGCTACTGCTTAAGACGGCTCGAAATTTCTACTGCGCGGACACAAATGAAGGC 262
|||||
.sProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
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.CCCCAATGTTGTTCTTGGTGTGGCAAGTCATATAAAGGCGCTAGACATTGCTATG 322
|||||
rAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
|||||
AGATATGTCCTGGAGAAAAGCGAAAGTAGTTATATACCCCTTCATTTCATACGGA 382
|||||
.sGluGlyTyrAlaGlnGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
|||||
.GGAAGGCTATGCAAGAGCGAAGATTCCACCGGATGCTACATTGATTTTGGATTGAA 442
|||||
uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
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TTATGCTGTGACCAAGGACCCAGGACATTGAGACATTTAAACAAATAGACATGGAC 502
|||||
nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
|||||
TGACAGCACTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAAGGGAATTTGAAAA 562
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pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
|||||
TGAGAAAGCCAGCGTGAACAGTCATATCAGGATGCGATTTTGAAGATATTTTAAAG 622
|||||
nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
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TGACCATGATGTTGTTGCTTCTTCTCCAGGATATACATGTATACCAACACAT 682
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uLeu 222
ACTA 688

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79 Application US/10013430A

US20030092883A1

RATION:

ker, Kevin P.
otstein, David
esnoyers, Luc
aton, Dan I.

errara, Napoleone

tong, Sherman

ao, Wei-Qiang

oddard, Audrey

odowski, Paul J.

rimaldi, Christopher J.

urney, Austin L.

illan, Kenneth J.

'an, James

'aoni, Nicholas F.

NTION: Secreted and Transmembrane Polypeptides and Nucleic

NTION: Acids Encoding the Same

IE: P2830PIC31

CATION NUMBER: US/10/013,430A

IG DATE: 2002-06-25

tion removed - See File Wrapper or Palm

ID NOS: 477

TYPE: DNA
ORGANISM: Homo sapiens
US-10-013-430A-179

Alignment Scores:

Pred. No.: 9,97e-148 Length: 907
Score: 1189.00 Matches: 222
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-013-430A-179 (1-907)

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QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuThr
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QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysLysGlu
Db 83 TTTACTGCTCAGACACAAAGAAAGAGGAGAGCACCAGAGAAAGTGAATAAGA
QY 41 HisArgProGluAAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
Db 143 CATGCTCCAGAAAACCTGCTCTAAGACAAAGCAAGAGGAGAGCCTACTAAATGC
QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
Db 203 GACGCTACCTGGCTTAAAGAGCGCTCGAAATTTCTACTGCGCGGACACAAA
QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
Db 263 CACCCCAATGCTTGTGTTCTTGGTGTGGCAAGTCATATAAAGGCGCTAGACAT
QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
Db 323 ACAGATATGTCCTCGAGAAAAGGCAAGTAGTTATACCCCTTCATTTGCG
QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
Db 383 AAGGAAGCTTATGCAAGAGGCAAGATTCCACCGGATGCTACATTGATTTTGA
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
Db 443 CTTTATGCTGTGACCAAGAGCACCAGGACATTGAGACATTTAAACAAATAGA
QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
Db 503 AATGACAGCGAGCTCTCTTAAAGCCGAGATAAACCTCTACTTGCAAAAGGGAATT
QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
Db 563 GATGAGAAAGCCAGCGTGAACAGTCATATCAGGATGCGATTTTAGAAGATATTTT
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
Db 623 AATGACCATGATGTGTGATGGCTTTCATTTCTCCAGAGGATATACATGTATACCA
QY 221 GluLeu 222
Db 683 GAACTA 688

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RESULT 13

US-10-011-671A-179
Sequence 179, Application US/10011671A
Publication No. US20030096954A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman

Gao, Wei-Qiang
Soddard, Audrey
Sodowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
ENTION: Secreted and Transmembrane Polypeptides and Nucleic
ENTION: Acids Encoding the Same
CB: P2830P1C27
ICATION NUMBER: US/10/011.671A
NG DATE: 2002-06-10
ATION NUMBER: 60/098716
DATE: 1998-09-01
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PRIORITY APPLICATION NUMBER: 60/102331
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PRIORITY APPLICATION NUMBER: 60/102484
PRIORITY FILING DATE: 1998-09-30
PRIORITY APPLICATION NUMBER: 60/102487
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 ATION NUMBER: 60/105002
 DATE: 1998-10-20
 ATION NUMBER: 60/105104
 DATE: 1998-10-21
 ATION NUMBER: 60/105169
 DATE: 1998-10-22
 ATION NUMBER: 60/105266
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 ATION NUMBER: 60/105693
 DATE: 1998-10-26
 ATION NUMBER: 60/105694
 DATE: 1998-10-26
 ATION NUMBER: 60/105807
 DATE: 1998-10-27
 ATION NUMBER: 60/105881
 DATE: 1998-10-27
 ATION NUMBER: 60/105882
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

Length: 907
 Matches: 222
 Conservativity: 0
 Mismatches: 0
 Indels: 0
 Gaps: 14

80 (1-222) x US-10-011-671A-179 (1-907)

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 TACTGCTCAGACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142
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Db 263 CACCCCAATGGTTTCTTGGTGGCAAGTCATATAAGGCCTAGACAT
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCTGGAGAAAAGCGAAAGTAGTTATATACCCCTTCATTTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGl
 Db 383 AAGGAAGGCTATGCAGAGGCGCAAGATTCCACCGGATGCTACATTGATTTTGA
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGAGACCGAGGCAITGAGACATTTAAACAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCNAAGGGAATT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCACGCGTGAAGTCATATCAGGATGCGAGTTTATAGAGATATTTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
 Db 623 AATGACCATGATGGTGGTGGCTTCATTTCTCCCAAGGAATACATGTATACCA
 QY 221 GluLeu 222
 Db 683 GAACTA 688

RESULT 14

US-10-012-755A-179

; Sequence 179, Application US/10012755A

; Publication No. US20030096955A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paori, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830PIC28

; CURRENT APPLICATION NUMBER: US/10/012.755A

; CURRENT FILING DATE: 2002-06-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 179

; LENGTH: 907

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-755A-179

Alignment Scores:

Pred. No.: 9.97e-148 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-012-755A-179 (1-907)

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 TTACTGCTCAGAGACAAAGAAAGAGGAGAGACCGAAGAAAGTGAATAAGAGTTTG 142
 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
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 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
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 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 TACCCAAATGGTTTGTTCATTGGTGTGGGCAAGTCATAAAAGGCGCTAGACATTGCTATG 322
 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
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 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 TAGGAAGGCTATGCAGAAAGCAAGATCCACCGGATGCTACATTGATTTTGAGATTGAA 442
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 TATGACAGGAGCTCTTAAAGCGAGATAAACCTCTACTTGCANAAGGGAATTGAAAA 562
 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
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 iluLeu 222
 TTTT
 TAACTA 688

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179 Application US/10015386A
180 Io. US2003009625A1
181 NATION:
182 Baker, Kevin P.
183 Botstein, David
184 Desnoyers, Luc
185 Eaton, Dan I.
186 Ferrara, Napoleone
187 Fong, Sherman
188 Gao, Wei-Qiang
189 Goddard, Audrey
190 Godowski, Paul J.
191 Grimaldi, Christopher J.
192 Gurney, Austin L.
193 Hillan, Kenneth J.
194 Pan, James
195 Paoni, Nicholas F.
196 /ENTION: Secreted and Transmembrane Polypeptides and Nucleic
197 /ENTION: Acids Encoding the same
198 ICE: P2830P1C55
199 IICATION NUMBER: US/10/015,386A
200 NG DATE: 2001-12-12
201 ation removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 179
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-386A-179

Alignment Scores:
Pred. No.:          9,97e-148          Length:          907
Score:             1189.00           Matches:         222
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:       100.00%            Indels:         0
DB:                14                 Gaps:           0

US-10-015-480A-180 (1-222) x US-10-015-386A-179 (1-907)

Qy 1 MetProLysThrMetHisPheLeuPheAArgPheIleValPhePheTyrLeuTf
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Qy 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleG
Db 83 TTTACTGCTCAGAGACAAAGAAAGAGCAGAGCACCGAAGAAAGTCAAAATAG
Qy 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
Db 143 CATCGTCCAGAAACTGCTCTAAAGCAAGCAAGAGGAGGACCTACTAAATG
Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
Db 203 GACGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGCAGCGCAGACAAAT
Qy 81 HisProLysThrPheValLeuGlyValGlyGlnValLleLysGlyLeuAspI
Db 263 CACCCCAATGGTTTGTTCITGGTGTTGGGCAAGTCATAAAGAGGCTAGACA
Qy 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
Db 323 ACAGATAATGTCCTGGAGAAAGCGAANAAGTAGTTATACCCCTTCATTGT
Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
Db 383 AAGGAAGGCTATGCAGAAAGGCAAGATCCACCGGATGCTACATGATTTTTG
Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
Db 443 CTTTATGCTGACCAAGGACCCAGGAGCATTGAGACATTTAAACAAATAG
Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPi
Db 503 AATGACAGGCAGCTCTCTAAGCCGAGATAAACCTCTACTTGCAAAGGGAAT
Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePi
Db 563 GATGAGAAGCCACGTGCAAGTCATATCAGGATGCAGTCTTTTAGAAGATATTT
Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
Db 623 AATGACCATGATGATGGCTTCATTTCTCCCAAGGAATACATGATATACC
Qy 221 GluLeu 222
Db 683 GAACCTA 688

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Search completed: April 9, 2004, 13:29:29
Job time : 2273 secs

: 10:32:16 2004

us-10-015-480a-180.rst

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame_plus_p2n model

April 9, 2004, 10:39:09 ; Search time 3101 Seconds
(without alignments)
2137.828 Million cell updates/sec

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1189
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

27513289 seqs, 14931090276 residues
hits satisfying chosen parameters: 55026578
length: 0
length: 2000000000
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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) spool/US10015480/runat_07042004_080125_28504/app_query.fasta_1.391
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RT=1 -ENDS=1 -MATRIX=biosum62 -TRANS=human40.gdi -LIST=45
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) OP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
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8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gsa_hum.*
18: em_gsa_inv.*
19: em_gsa_pln.*
20: em_gsa_vrt.*
21: em_gsa_fun.*
22: em_gsa_mam.*
23: em_gsa_mus.*
24: em_gsa_pro.*
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26: em_gsa_pbg.*
27: em_gsa_vrl.*
28: gb_gsa1.*
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29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1146	96.4	786	14	CF593540	CF593540
3	1145	96.3	807	14	CB989909	CB989909
4	1121	94.3	780	12	BI827688	BI827688
5	1085	91.3	643	12	CG939266	CG939266
6	1079	90.7	943	14	CD557479	CD557479
7	1010	85.0	734	10	BE874396	BE874396
8	936	78.8	734	14	CB570987	CB570987
9	935	78.6	618	14	CF794142	CF794142
10	929	73.1	602	13	BUS51693	BUS51693
11	908	76.4	602	13	BA485892	BA485892
12	890	74.9	800	14	CB959508	CB959508
13	865	72.8	604	12	BI964616	BI964616
14	856	72.0	644	12	CG896952	CG896952
15	837	70.4	673	9	AI182368	AI182368
16	832	70.0	546	10	BE756310	BE756310
17	817	68.7	861	13	BU400194	BU400194
18	817	68.7	922	13	BU135960	BU135960
19	813	68.4	884	13	BU253965	BU253965
20	809	68.0	647	13	BU300409	BU300409
21	805	67.7	769	13	BU319076	BU319076
22	803	67.6	748	14	CB573983	CB573983
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26	799	67.2	856	13	BU405087	BU405087
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28	790	66.5	553	14	CF112806	CF112806
29	786	66.1	1026	13	BU356231	BU356231
30	783	65.9	498	9	AA457921	AA457921
31	772	64.9	643	14	CF792774	CF792774
32	771	64.8	521	9	AW082138	AW082138
33	766	64.5	699	14	CF794309	CF794309
34	764	64.3	889	13	BU359419	BU359419
35	760	64.0	457	9	AI879695	AI879695
36	760	63.9	811	10	BF210667	BF210667
37	753	63.3	893	13	BU128923	BU128923
38	747	62.8	755	13	BU136444	BU136444
39	745	62.7	517	9	AV745382	AV745382
40	734	61.7	550	13	BX515852	BX515852
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42	719	60.5	506	10	BE850956	BE850956
43	717	60.3	775	13	BU299669	BU299669
44	712	59.9	636	14	CA313338	CA313338
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ALIGNMENTS

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LOCUS AF092137 1231 bp mRNA linear HTC
DEFINITION Homo sapiens FK506-binding protein mRNA, complete cds.
ACCESSION AF092137
VERSION AF092137.1 GI:5138923
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor
REFERENCE 1 (bases 1 to 1231)
AUTHORS Han,Z., Song,H., Dai,M., Huang,Q., Mao,Y., Zhang,Q., Mac
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M., Chen, J. and Hu, R.
 an FK506-binding protein mRNA, complete cds
 (bases 1 to 1231)

ect Submission
 mitted (16-SEP-1998) Shanghai Second Medical University, Rui-Jin
 pital, Shanghai Institute of Hematology, 197 Rui-Jin Road II,
 ngshai 200025, P.R. China
 Location/Qualifiers

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 ity: 100.00% Conservative: 1
 arity: 99.55% Mismatches: 0
 99.58% Indels: 0
 11 Gaps: 0

180 (1-222) x AF092137 (1-1231)

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LOCUS
 DEFINITION AGENCOURT 15624003 NIH MGC 147 Homo sapiens cDNA clone
 IMAGE:30531031 5', mRNA sequence.

ACCESSION CF593540

VERSION CF593540.1 GI:36347183

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; HC

REFERENCE 1. (bases 1 to 786)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collectic

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI

DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution informatio

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM621 row: c column: 08

High quality sequence stop: 623.

Location/Qualifiers

source

1. .786

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insert size 2.3 kb and normalized to ROT 5. T

primary library enriched for full-length clone

constructed using the Cap-trapper method (Car

preparation). Library constructed by M. Brown

(NIH/NHGRI, National Institutes of Health). X

a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 2,78e-115 Length: 786

Score: 1146.00 Matches: 221

Percent Similarity: 98.67% Conservatives: 1

Best Local Similarity: 98.22% Mismatches: 0

Query Match: 96.38% Indels: 3

DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x CF593540 (1-786)

atProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
 |||||
 GCACAAACCATGATCTTATTCAGATTCATTTCTTTTATCTGTTGGGCTTT 160
 |||||
 leThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
 |||||
 TACTGCTCAGACACAAAGAGGAGAGACCCGAAAGAGTGAATAGAGTTTGG 220
 |||||
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 |||||
 TCGTCCAGAAACCTGCTTAAGACAAGCAAGAGGAGACCTACTAATGCCATAT 280
 |||||
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 |||||
 CGGCTACTCGCTAAAGACGGCTCGAAATTTCTACTGACGGGACACAAATGAAGC 340
 |||||
 sProLysTyrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 |||||
 CCCCNAATGTTGTTCTTGGTGGGCAAGTCATAAAGGCTGACATTGCTATG 400
 |||||
 rAspMetCysProGlyLysArgLysValIleProProSerPheAlaTyrGly 120
 |||||
 AGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCATACGA 460
 |||||
 sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluLeu 140
 |||||
 GGAAGGCTATGCGAAGGCGAAGATTCACCGGATGCTACATTGATTTTGAATGAA 520
 |||||
 uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 |||||
 TTATGCTGTGACCAAGGACACGAGCATTGAGACATTTAAACAAATAGACATGAC 580
 |||||
 nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 |||||
 TGACAGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTCGAAAGGGAATTCGAAA 640
 |||||
 pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIle-PheLysIly 200
 |||||
 TGAGAAGCCACGTCGACAAAGCATATCAGGATGCGAGTTTGTAGAGATATTTTAA 700
 |||||
 snAspHisAspGlyAsp-GlyPheIleSerProLysGluTyrAsnValTyr-GlnHis 219
 |||||
 ATGACCATGATGTGTGTTGCTTCATTTCTCCCAAGATACAAATGTATACCAACAC 760
 |||||
 pGluLeu 222
 |||||
 TGAACATA 769

9909 787 bp mRNA linear EST 01-MAY-2003
 COURT_13903492 NIH MGC 147 Homo sapiens cDNA clone
 E:30341652 5', mRNA sequence.

9909.1 GI:30284429

sapiens (human)

sapiens
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 bases 1 to 787)

MGC <http://mgi.nci.nih.gov/>.

onal Institutes of Health, Mammalian Gene Collection (MGC)
 blished (1999)

act: Robert Strausberg, Ph.D.

l: cgapbs-remail.nih.gov

ue Procurement: Dr. Stefan Hansson

A Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)

A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Agencourt Bioscience Corporation

ae distribution. MGC clone distribution information can be

d through the I.M.A.G.E. Consortium/LLNL, at:

<http://image.llnl.gov>
 Plate: NDAM373 row: h column: 13
 High quality sequence stop: 621.

FEATURES

source
 1..787
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30341652"
 /tissue_type="Human Placenta"
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 /clone_lib="NIH MGC 147"
 /note="organ: placenta; Vector: pBluescriptR;
 all-XhoI; Site 2: BamH; Oligo-dT primed using
 5'-TTTTTCTTTTCTTTTNN-3', size-selected for a
 insert size 2.3 kb and normalized to 10⁵ 5' th
 primary library enriched for full-length clone
 constructed using the Cap-trapper method (Car
 preparation). Library constructed by M. Brown
 (NIH/NHGRI, National Institutes of Health). M
 a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,59e-115 Length: 787
 Score: 1145.00 Matches: 219
 Percent Similarity: 98.65% Conservative: 1
 Best Local Similarity: 98.21% Mismatches: 1
 Query Match: 96.30% Indels: 2
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x CB989909 (1-787)

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 Db 100 ATGCCAAACCATGATCTTATTCAGATTCATTTCTTTTATCTGTTGG 219
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 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGln 1
 |||||
 Db 160 TTTACTGCTCAGACACAAAGAGAGGAGACCCGAAAGAGTGAATAGAG 1
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 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla 1
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 Db 220 CATCGTCCAGAAACCTGCTCTAAGACAAGCAAGAGGAGGAGACCTACTAAATG 1
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 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGluAsp 1
 |||||
 Db 280 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACGGCGACACAAA 1
 |||||
 QY 81 HisProLysTyrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle 1
 |||||
 Db 340 CACCCCAATGTTGTTCTTGTGTTGGCAAGTCATATAAGGCGCTAGACATT 1
 |||||
 QY 101 ThrAspMetCysProGlyGluLysArgLysValIleProProSerPheAla 1
 |||||
 Db 400 ACAGATATGTGCCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCA 1
 |||||
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu 1
 |||||
 Db 460 AAGGAAGGCTATGCGAAGGCGAAGATTCACCGGATGCTACATTGATTTTGG 1
 |||||
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsp 1
 |||||
 Db 520 CTTTATGCTGTGACCAAGGACCCGAGGAGCATTTGAGACATTTAAACAAATAG 1
 |||||
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe 1
 |||||
 Db 580 AATGACAGGCGAGCTCTCTAAAGCGGAGATTAACCTCTACTTGTGCAAGGGA 1
 |||||
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe 1
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 Db 640 GATGAAGAGCCGCTGACAAAGTCATATCATGAGTGCAGTCTTTTAGAAGATA 1
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snAspHisAspGlyAspGlyPheIleSer-ProLysGluTyrAsnValTyr-GlnHisA 220
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dGlu 221
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 TGAA 764

27688 800 bp mRNA linear EST 04-OCT-2001
 074295F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166166 5',
 A sequence.

27688
 27688.1 GI:15939238

o sapiens (human)

o sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 800)

-MGC http://mgi.nci.nih.gov/.

ional Institutes of Health, Mammalian Gene Collection (MGC)

ublished (1999)

tact: Robert Strausberg, Ph.D.

il: cgabs-remail.nih.gov

sue Procurement: Life Technologies, Inc.

NA Library Preparation: Life Technologies, Inc.

A Sequencing by: The I.M.A.G.E. Consortium (LLNL)

one distribution: MGC clone distribution information can be

nd through the I.M.A.G.E. Consortium/LLNL at:

p://image.llnl.gov

h quality sequence stop: 794.

Location/Qualifiers

1. .800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5166166"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

s:

1.38e-112 Length: 800

1121.50 Matches: 220

ity: 98.21% Conservative: 0

larity: 98.21% Mismatches: 1

94.32% Indels: 4

12 Gaps: 1

180 (1-222) x B1827688 (1-800)

letProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20

|||||

TGCCAAAACCAACGCAATTCATTATTCAGATTCATTTCTTTTATCTGTGGGGCCTT 139

|||||

hethrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40

|||||

TTACTGCTCAGACACAAAGAAAGAGAGAGACCCAGAGAGAGTGAATAGAGACT-TTG 198

QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
 |||||
 Db 199 CATCGTCCAGAAACTGCTCTTAGACAAGCAAGAGGAGACCTACTAATG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 |||||
 Db 259 GACGGCTACCTGGCTAAAGACGGCTGAAATTTCTACTGCAGCGGACACAAA
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspI
 |||||
 Db 319 CACCCCAATGGTTTGTCTTGGTGTGGCAAGTCAATAAAGCCCTAGACA
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProSerPheA
 |||||
 Db 379 ACAGATATGTCCCTGGAGAAAAGCGAAAGTAGTTATATACCCCTTCATTG
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 |||||
 Db 439 ARGGAAGGCTAT--GAAGCAAGATTCACCGGATGCTACATTGATTTTGT
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
 |||||
 Db 496 CTTTATGCTGTGACCAAGAGACCCAGGAGCATTTAGACATTTAAACAAATAG
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
 |||||
 Db 556 AATGACAGGCAGCTCTTAAAGCCGAGATAAACCTCTACTTGCAGAGGAATT
 QY 181 AspGluLysProArgAspLysSerTyr-GlnAspAlaValLeuGluAspIle
 |||||
 Db 616 GATGAAGAGCCAGCTGACAGTCATATCCAGGATGCAGTTTATAGAGATATT
 QY 200 sAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyr-AsnValTyr
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 Db 676 GATGACCATGATGTGTGCTTCATTCTCCCAAGGATACAAATGATATAC
 QY 220 spGluLeu 222
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 Db 736 ATGAACATA 743

RESULT 5

BG939266

LOCUS

DEFINITION

clone NTBC_cn31e10 random, mRNA sequence.

ACCESSION

BG939266

VERSION

BG939266.1 GI:14338638

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,

Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang

Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.

SGAP: The Skeletal Genome Anatomy Project

Unpublished (1997)

CONTACT: Libin Jia

Medical Genetics Branch

National Human Genome Research Institute

10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267

Tel: 301-402-4877

Fax: 301-496-7157

Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of H

Intramural Sequencing Center (NISC).

Plate: 31 row: e column: 10

Seq primer: -21M13 forward primer (ABI).

FEATURES

Location/Qualifiers

1..643

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="NHTBC_cnl1e10"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site 1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)"

SI: 1.1e-108 Length: 643
ity: 1085.00 Matches: 204
larity: 100.00% Conservativity: 0
91.25% Mismatches: 0
12 Indels: 0
Gaps: 0

180 (1-222) x BG939266 (1-643)

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GCCTTTTACTGCTCAGACACAAAGAAAGAGAGAGACCCGAGAGAGTGAATAGAA 68
alLeuHisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla 58
TTTTGCATCGTCAGAAAACCTGCTTAAGACAGCAGAGAGAGAGACCTACTAAATGCC 128
isTyrAspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsn 78
ATTATGACGGCTACCTGGCTTAAGACGGCTCGAAATTTCTACTGCAGCGGACACAAAT 188
luGlyHisProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIle 98
AAGCCACCCCAATAGTTTGTCTTGGTGGGCAAGTCATAAAGGCGCTAGACAT 248
laMetThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla 118
TATGACAGATATGTGCTGAGAAAGCGAAAGTAGTTATACCCCTTCATTGCA 308
TGlyLysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu 138
ICGGAAGAGAGAGGCTATGAGAAAGCAAGATCCACCGGATGCTACATTTTGTAG 368
eGluLeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsp 158
TGAACCTTATGCTGTGACCAAGAGCAGCAGGACATTCAGACATTTAAACAAATAGAC 428
tAspAsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe 178
GGCAATGACAGGCGAGCTCTTAAGCCGAGATAAACCTCTACTTGAAGGAAATTT 488
uLysAspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe 198
AAAGATGAGAACCCAGCTGACAGTCAATATCAGGATGCGATTTTGAACATATTTT 548
sLysAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGln 218
GAAGATGACCATGATGGTGTGCTTCATTTCTCCCAAGGAATACAAATATATACCA 608
sAspGluLeu 222
CGATGAACATA 620

7479 943 bp mRNA linear EST 11-JUN-2003
COURT 14413656 NIH MGC 180 Homo sapiens cDNA clone
E:30387633 5', mRNA sequence.
7479
7479.1 GI:31583547

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 943)
NTH-MSC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collecti
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabps-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LI
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM458 row: d column: 10
High quality sequence stop: 601.

FEATURES
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/clone="IMAGE:30387633"
/lab_host="DH10B-Ton A (T1 and T5 phage resis
/notes="Organ: testis; Vector: pCMV-SPORT6.1; S
Site 2: EcoRV (destroyed); Library is oligo-di
directionally cloned (EcoRV site is destroyed
cloning). Average insert size 1.68 kb. Library
constructed by (Invitrogen). Note: this is a N
Library."

ORIGIN

Alignment Scores:
Pred. No.: 7.5e-108 Length: 943
Score: 1079.00 Matches: 211
Percent Similarity: 97.26% Conservative: 2
Best Local Similarity: 96.33% Mismatches: 4
Query Match: 90.75% Indels: 2
DB: 14 Gaps: 0
US-10-015-480a-180 (1-222) x CD557479 (1-943)
QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
Db 92 ATGCCAAACCATCATCTTCTTATTCAGATTCAATTTCTTTTATCTGTG
QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
Db 152 TTTACTGCTCAGACAAAGAAAGAGAGAGAGACCCGAGAGTGAATAGAG
QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl
Db 212 CATGCTCCAGAAAACCTGCTTAAGACAGCAAGAGAGAGACCTTACTAGTGC
QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsi
Db 272 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACGCGACAAAA
QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspIle
Db 332 CACCCCAATGTTTGTCTTGGTGGTGGCAAGTCATAAAGGCGCTAGACAT
QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
Db 392 ACAGATATGTCCTCGAGAGAAAGCAAGAGTAGTTATACCCCTTCAATTGCP

LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 AAGGAAGGCTATGCAGAGGCAAGATTCCACCGATGCTACATGATTTTTCAGATTGAA 511
 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
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 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 AATGACAGGACGCTCTTAAGCCGAGATAAACCCTACTTGCRAAGGGAATTTGAAAAA 631
 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAsp-IlePheLysIly 200
 ATAGAGAGCCACGTCACAAAGTCATATCAGGATGCGAGTTTATAGAGAATATTTTAAANA 691
 AsnAspHisAsp-GlyAsp-GlyPheIleSer-ProLysGluTyrAsn 215
 ATATGACCATGATGGGTGATGGGCTTCATTTCTCCCCAGGGAATACAAT 740

374396 734 bp mRNA linear EST 20-OCT-2000
 148821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891173 5',
 VA sequence.

374396
 374396.1 GI:10323172

no sapiens (human)
 no sapiens
 caryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 amalia; Eutheria; Erimates; Catarrhini; Hominidae; Homo.
 (bases 1 to 734)
 i-MGC <http://mgi.nci.nih.gov/>.
 ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 tract: Robert Strausberg, Ph.D.
 il: cgabbs-remail.nih.gov
 issue Procurement: DCTD/BTP/Gazdar
 NA Library Preparation: Life Technologies, Inc.
 NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 A Sequencing by: Inyte Genomics, Inc.
 one distribution: MGC clone distribution information can be
 und through the I.M.A.G.E. Consortium/LLNL at:
 p://image.llnl.gov
 ite: LAM9675 row: j column: 06
 ph quality sequence stop: 602.
 Location/Qualifiers

1..734
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3891173"
 /tissue_type="large cell carcinoma, undifferentiated"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_69"
 /note="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

si:
 1.88e-100 Length: 734
 1010.50 Matches: 203
 ity: 92.41% Conservative: 4
 larity: 90.62% Mismatches: 11
 84.99% Indels: 6
 10 Gaps: 1

180 (1-222) x BE874396 (1-734)

etProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20

Db |||||
 31 ATGCCAAAACCATGCAATTTCTATCAGATTCATGTTTCTTTATCTGT
 QY |||||
 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleG
 Db |||||
 91 TTTACTGCTCAGAGACAAAAGAAAGAGAGAGACCGGAAGATGAAATAG
 QY |||||
 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuAsnA
 Db |||||
 151 CATGCTCCAGAAAACCTGCTCTAAGACAAGCAAGAGAGGAGACCTACTAAATG
 QY |||||
 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 Db |||||
 211 GACGCTACCTGGCTTAAGAGCGCTCGAAATTTCTACTGAGCGGACACAAA
 QY |||||
 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
 Db |||||
 271 CACCCCAATGGTTGTTCTTGGTGTGGGCAAGTCATAAAAGGCTTAGACA
 QY |||||
 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 Db |||||
 331 ACAGATATGTGCCCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTG
 QY |||||
 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIle-Phe
 Db |||||
 391 AAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATGATTTCTT
 QY |||||
 140 uLeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIle
 Db |||||
 451 ACTTTATGCTGTGACCAAAAGGACCGAGCATTCAGACATTTAAACAAATA
 QY |||||
 160 pAsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGlu
 Db |||||
 511 CAATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGGA
 QY |||||
 180 sAspGluLysProArgAsp-LysSerTyrGlnAspAlaValLeuGluAsp-I
 Db |||||
 571 AGATGAGAGCCACGTCAGACRAGTCATATCAGGATGCGATTCACAGACTA
 QY |||||
 200 LysAsnAspHis-Asp-GlyAspGlyPhe---IleSerProLysGluTyrAs
 Db |||||
 631 ACCACTGACCATCGATCGGAATGCCCTTCCATTTCTCCCGACGGAATTACAC
 QY |||||
 218 ln 218
 691 AA 692

RESULT 8
 CB570987
 LOCUS
 DEFINITION
 CB570987 734 bp mRNA linear EST
 AGENCOURT 12993310 NIH_MGC_165 Mus musculus cDNA clone
 IMAGE:30278220 5', mRNA sequence.

ACCESSION
 VERSION
 CB570987
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M

REFERENCE
 1 (bases 1 to 734)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collectic
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Leslie L. Heckert
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM32 row: e column: 13

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1 quality sequence stop: 566.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
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/clone_lib="NIH_MGC_165"
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(ggcatatggcc); Site_2: sfii (ggcgctcgcc); 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATGCGC-3' and 3' adaptor
sequence: 5'-ATCTAGACCGCAGCGCGCAGC-AT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0.6-3.5 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."

;:      2,45e-92      Length:      734
      936.50      Matches:      180
ty:      89.20%      Conservative:      10
arity:      84.51%      Mismatches:      21
      78.76%      Indels:      2
      14      Gaps:      1

80 (1-222) x CB570987 (1-734)

tHisPheLeuPheArgPheIleValPheTyrLeuTyrGlyLeuPheThrAlaGln 24
GAATCTCTATTTCAGATAGCAGTTTCTTCCTAGCTGTGTGTGTTCGATGCTCAG 95

gGlnLYsGLuGLuSerThrGlnGLuValLYsIIEGLuValLeuHisArgProGlu 44
ACAAACAAAGAGAGAAAGCACTGAGGAGTGAATAAGTAGAAGTTTGCACGTCAGAA 155

nCySerLYsThrSerLYsGLyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeu 64
CTGCTCCAAACAAAGCAGGAAAGAGACTTGCTAAATGCCATTACGATGGCTACTTG 215

aLYsAspGLySerLYsPheTyrCySerArgThrGlnAsnGLuGlyHisProLYsTyr 84
TAAAGACGGCTCCAAATTTCTACTGCGAGCGGACACAGATGAAGGCCACCCCAATGG 275

eValLeuGLyValGLyGlnValIleLYsGLyLeuAspIleAlaMetThrAspMetCys 104
TGTTCITGTGTGCGACATGTCATAAAGGGCTGGACATTCCTATATGATGGATGGC 335

oGLyGLuLYsArgLYsValValIleProSerPheAlaTyrGLyLYsGLuGLyTyr 124
TGGGGAAGAAAGAGAAAGTGATATATACCGCTTCGTTTGATATGAAAGAGGCTAC 395

aGLuGLyLYsIIEProProAspAlaThrLeuIlePheGluIIEGLuLeuTyrAlaVal 144
AGAAGCAAGATTCACCAACCAATGCAACTCTGATGTTTGAGATTGAACCTTATGCTGTG 455

rLYsGLyProArgSerILEuThrPheLYsGlnIIEAspMetAspAsnAspArgGln 164
CAAGACCAAGAGGAGATTGAACATTTAAGCAAAATAGACACGGAATAATGACCGGCAA 515

uSerLYsAlaGLuIIEAsnLeuTyrLeuGlnArgGluPheGluLYsAspGluLYsPro 184
CTCCAAAGCTGAGATAGACTTTACTTACAGAGAGACTTTGAAAAGATGCAAAACCCC 575

zAspLYsSerTyrGlnAspAlaValLeuGluAspIIEPheLYsLYsAsnAspHisAsp 204
TGAACAAGTCATATCAAAAGCAGTTTGGAGATATCTTTAAGAAAAATGACCAACAT 635

lyAspGLyPhe---IIESerProLYsGluTyrAsn 215

```


ispMetCysProGlyGluLysValValleProProSerPheAlaTyrGlyLys 121
 :ATATGTCCTGGAGAGAGCGAAAGTGATTATACCCCTCTCTTTCATATGGAAG 398
 :luGlyTyrAlaGluGlyValleProProAspAlaThrLeuLeuPheGluLeu 141
 :AAGCTATGAGAGAAAGCAAGATTCACCTAATGCAACATTGATTTTGGAGATTGAACCT 458
 :YzAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsn 161
 :ATGCTGTAAACCAAGGACCGACGACGATTGAACATTTAAACAGATAGACCGACAAT 518
 :aspArgGlnLeuSerLysAlaGluLeuLeuTyrLeuGlnArgGluPheGluLysAsp 181
 :ACAGACAACTCTCTAAACCTGAGATAAATCATTAACCTGAAAGAAAGGATTTGAAAGAT 578
 :luLysProArgAspLysSerTyrGlnAspAlaValleu 194
 :AGAGCCACGTCGACAAATCATATCAGAAATGACGTTTGA 617

51693 602 bp mRNA linear EST 16-SEP-2002
 19c12.y1 McCarrey Eddy type A spermatogonia Mus musculus CDNA
 ne IMAGE:8442846 5' similar to TR:054998 OS4998 FK506-BINDING
 TEIN. ; mRNA sequence.
 51693
 51693.1 GI:22934554

musculus (house mouse)
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 602)
 arrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
 tin,J., Wylie,T., Dente,M., Bowers,Y., Theising,B., Gibbons,M.,
 ter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
 nett,J., Waterston,R. and Wilson,R.
 HS Mouse
 ublished (2002)
 tact: McCarrey/Eddy NIEHS Mouse
 HS Mouse
 hington University School of Medicine
 4 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 : 314 286 1800
 : 314 286 1810
 il: est@watson.wustl.edu
 s clone is available royalty-free through LLNL ; contact the
 GE Consortium (info@image.llnl.gov) for further information.
 :2067958
 primer: -40RP from Gibco
 h quality sequence stop: 421.
 Location/Qualifiers
 1. 602
 /organism="Mus musculus"
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 /db_xref="taxon:10090"
 /clone="IMAGE:6442846"
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 mice"
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 (Stratagene); Site 1: XhoI; Site 2: EcoRI; CDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTTT-3'] and
 directionally cloned using 5' linkers 5'-AATTCCGACAG-3'
 and 5'-CTGTCGCG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-UniZAP-XR) and resulting

single-stranded phagemids were prepped and tr.
 into DH10B. Library contains 96.5% recombinan
 References: J. Androl. 20:635-639 and Gene 25
 Library constructed and donated by J. McCarre
 (Southwest Foundation for Biomedical Research
 Genetics); excision done by E.M. Eddy, Ph.D.
 Institutes of Health, National Institute of I
 Health Sciences). Original lambda-based libr
 available through ATCC, catalog #63416."

ORIGIN

Alignment Scores:
 Pred. NO.: 1.32e-91 Length: 602
 Score: 929.00 Matches: 175
 Percent Similarity: 91.50% Conservative: 8
 Best Local Similarity: 87.50% Mismatches: 17
 Query Match: 78.13% Indels: 0
 DB: 13 Gaps: 0

US-10-015-480A-180 (1-222) x BU551693 (1-602)

QY 8 LeuPheArgPheIleValPhePheTyrLeuTyrGlyLeuPheThrAlaGlnA
 :|||||
 Db 2 CTATTCAGACTAGCAGTTTCTTAGCCTGTGGTGTGTTCGCGATGCTCAGG
 :|||||
 QY 28 LysGluGluSerThrGluGluValLysIleGluValLeuHisArgProGluA
 :|||||
 Db 62 AAAGAGAAAGCCTGAGGAAGTGAATAAGAGTTTTCACCGTCCAGAA
 :|||||
 QY 48 LysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeuA
 :|||||
 Db 122 AAAACAAGCAGGAAAGAGAGACTTGTCTAAATGCCCATTTACGATGGCTACTTGG
 :|||||
 QY 68 GlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisProLysTyrP
 :|||||
 Db 182 GGTCTCCAAATTTCTACTGACGCGACACAGATGAAGGCCACCCCAATGGT
 :|||||
 QY 88 GlyValGlyGlnValIleLysGlyLeuAspIleAlaMetThrAspMetCysP
 :|||||
 Db 242 GGTGTGGACATGTCTATAAGGGGGCTGGACATTTGCTATGATGACATGTGCC
 :|||||
 QY 108 LysArgLysValValIleProProSerPheAlaTyrGlyLysGluGlyTyrAl
 :|||||
 Db 302 AAGAGAAAGTGATTTATACCTCTTCATTTGCATATGGAAGAAAGGCTATGC
 :|||||
 QY 128 LysIleProProAspAlaThrIleuIlePheGluIleGluLeuTyrAlaValT
 :|||||
 Db 362 AAGATTCACCCCAATGCAACTCTGTATGTTTGAATGAACCTTATGCTGTGAC
 :|||||
 QY 148 ProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAspArgGlnL
 :|||||
 Db 422 CCAAGGAGCATTTGAACATTTAAGCAAAATAGACACCGATAATGACCGCACT
 :|||||
 QY 168 AlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLysProAr
 :|||||
 Db 482 GCTGAGATAGAGCTTTTACTTTACAGAGGAGCTTTGAAAAAGATGCAAAACCCCG
 :|||||
 QY 188 SerTyrGlnAspAlaValLeuGluAspIlePheLysLysAsnAspHisAspGl
 :|||||
 Db 542 TCATATCAGAGCGACGCTTTTGGAGATATCTTTTAAGAAAAAATGACCACCAATGG
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RESULT 11

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 DEFINITION
 DXFP2686C11249_r1 686 (synonym: hlccc3) Homo sapiens CDN
 DXFP2686C11249_5', mRNA sequence.
 ACCESSION
 EX485892
 VERSION
 EX485892.1 GI:31949079
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Hom

[illegible]

```

TATCGTCAGAAACTGCTTAAGACAGCAAGCAAGAGGAGACCTACTAAATGCCCATTTAT 279
aspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
HACGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGACGGGACACAAAATGAAGGC 339
hisProLysTyrPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100
ACCCCAATGGTTGTTCTTGGTGTGGCAAGTCATAAAGAGGCTAGACATTGCTATG 399
hrAspMetCysProGlyGluLysArgLysValValLysProProSerPheAlaTyrGly 120
CAGATATGTCCTCGGAAAGAGGAAAGTAGTATTACCCCTTATTTCATACGGA 459
ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
AGGAAGCTATGACGAAGGCAAGATCCCGCCGATGCTACATTGATTTTGATTTGAA 519
euTyrAlaValThrLysGlyProArgSerTleGluThrPheLysGlnIleAspMetAsp 160
TTTATGCTGTGACCAAGGACCAAGGACGAACTTGAACATTTAAACAAATAGACCTGGAC 579
snAspArgGlnLeuSerLysAla--GluIleAsnLeu-Tyr-LeuGlnArgGluPhe-- 178
ATGACAGGAGCTCTTCTTAAGCCCGGAAATTAACCTCTCTTGTGAAAGGGAATTTTG 639
GluLysAspGluLysProArgSerLysTyrGlnAspAlaValLeuGluAspIlePhe 198
AAAAAATGAGAAACCCACGCTTGACAAAGTGCCATATTTCAGGATG-----CAGGTTTT 693
LysLysAsn 201
:|||||
AGAAAAAT 703

64616      604 bp      mRNA      linear      EST 12-MAR-2002
0g11.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
culus cDNA clone IMAGE:5665748 5' similar to TR:054998 054998
64616
64616.1 GI:16339021
musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 604)
ton.D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
ishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
lier,I., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
natt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
enas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
iams,T., Jackson,Y. and Bowers,Y.
ocrine Pancreas Consortium
blished (2000)
ar_ESTs: id40g11.xl
act: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
ocrine Pancreas Consortium
ard University, Howard Hughes Medical Institute
: of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
02138
: 617-495-1812
: 617-495-8557
il: dmelton@biohp.harvard.edu
rary was constructed by Dr. Douglas Melton DNA sequencing by:
ingron University Genome Sequencing Center For information on
ining a clone please contact: Juliana Brown
jw@fas.harvard.edu)
:1952074 This sequence now available from the IMAGE consortium,
clone orders contact: info@image.llnl.gov
1 quality sequence stop: 427.
Location/Qualifiers

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source

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1. .604
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/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
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/sex="Both for embryonic & newborn, male for :
adult islet"
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adult, mixed"
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N1-MMS1"
/notes="Vector: pSPORT1; Site 1: Not I; Site 2:
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pancreas, newborn pancreas, adult pancreas, i
islets of Langerhans were separately construc
SuperScript plasmid library kit (Life Techno
was made by oligo-dT priming and size-selectec
fractionation. Libraries were amplified once c
support and plasmid DNA from each library was
and mixed in equal amounts. The mixed library
normalized by method #4 from Bonaldo, Lennon,
1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was
5 micrograms PCR product representing mixed li
inserts and hybridized to an EcoT of 6. Singl
(unhybridized) plasmids were isolated by hydr
chromatography and used to make this library.

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ORIGIN

```

Alignment Scores:
Pred. No.: 1 39e-84      Length: 604
Score: 865.00      Matches: 164
Percent Similarity: 90.53%      Conservative: 8
Best Local Similarity: 86.32%      Mismatches: 18
Query Match: 72.75%      Indels: 0
DB: 12      Gaps: 0

US-10-015-480A-180 (1-222) x BI964616 (1-604)

QY 5 MetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeuPheTh
Db :|||:|||||
35 ATGAATCTCTTATTCAGACTAGCAGTTTCTTAGCTGTGGTGTGTTCGGA
QY 25 ArgGlnLysGlyGluSerThrGluGluValLysIleGluValLeuHisAr
Db :|||:|||||
95 GGACAAACAAAAGAGAAAGACCTGAGGAAGTGAAAAATAGAAGTTTGCACCG
QY 45 AsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyrAspGI
Db :|||:|||||
155 AACTGCTCCAAACCAAGCAGGAGAGACTTGTCTAAATGCCCATTTACCATGG
QY 65 AlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisPr
Db :|||:|||||
215 GCTAAAGACGGCTCCAAATTTCTACTGACGCGGACACAGAATGAAGGCCACCC
QY 85 PheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMetThrAsi
Db :|||:|||||
275 TTGTGTTCTGTGGTGTGGACATGTCTATAAAGGGGCTGGACATTGCTATGATGA
QY 105 ProGlyGluLysArgLysValValLysProProSerPheAlaTyrGlyLysGln
Db :|||:|||||
335 CTTGGGGAAAGAGAAAGGTGATTATACCTCTCTTCAATTGCATATGGAAGAAG
QY 125 AlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGluLeuTy
Db :|||:|||||
395 GCAGAAGGCAAGATTCCACCCCAATGCAACTCTGATGTTTGTGATTTGAATTGA
QY 145 ThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAsi
Db :|||:|||||
455 ACCAAAGGACCAAGAGGCAATTGAACATTTAAGCAATAGACACGGAATATGA

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euSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLysPro 184
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TCTCCAAAGCTGAGTAGAGCTTTACTTACAGAGGAGCTTTGAAAAAGATGCAAGCC 574

rgAspLysSerTyrGlnAspAlaValLeu 194
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GTGACAAAGTCATATCAGAGGAGCTTTTG 604

96952 644 bp mRNA linear EST 06-NOV-2001
59-1-C9.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
96952 mRNA sequence.
36952.1 GI:14307193

; sapiens (human)
; sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
nalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 644)
r,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mac,J.,
e,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
t,M.W.
itification and initial characterization of 5000 expressed
enced tags (ESTs) each from adult human normal and
oarthritic cartilage cDNA libraries
oearth. Cartil. 9 (7), 641-653 (2001)
12651
17177
act: Sanjay Kumar
09
oSmithKline
Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
610-270-7245
610-270-5598
l: sanjay.kumar-1@gsk.com
primer: 77
Location/Qualifiers
1..644
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/lab_host="E.coli DH10 B"
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Directional"

: 1.44e-83 Length: 644
856.00 Matches: 164
ty: 98.80% Conservative: 0
arity: 98.80% Mismatches: 2
71.99% Indels: 1
12 Gaps: 0

30 (1-222) x BG96952 (1-644)

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TACTGCTCAGAGACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263
rArgProGluIleCysSerLysThrSerLysGlyAspLeuLeuAsnAlaHisTyr 60
CGTCCAGAAACCTGCTTAAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
rGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGly 80

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Db 324 GACGGCTACTGCTAAGACGCTCGAATTCCTATCGACCGGACACAAA
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Db 384 CACCCCAAAATGGTTTGTCTTGTGGCAAGTCATAAAGGCGCTAGACA
|||
QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProSerPheAl
|||
Db 444 ACAGATATGTCCTCGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGC
|||
QY 121 LysGluGlyTyrAlaGluGlyLysIleProAspAlaThrLeuIlePheGl
|||
Db 504 AAGGAGGCTATGCAGAGGCGAGATCCACCGGATGTACATGATTTTGA
|||
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
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Db 564 CTTTATGCTGTGAC-AAAGCACCAGGGGCGCATTTAGACATTTAAACAATAGA
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QY 161 AsnAspArgGlnLeuSer 166
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Db 623 AATGACAGCGACTCTCT 640
|||

RESULT 15
Al182368/c
LOCUS
DEFINITION
673 bp mRNA linear EST
IMAGE:1451065 3' similar to SW:FKB2_MOUSE P45878 FK506-
PROTEIN PRECURSOR ; mRNA sequence.
Al182368
Al182368.1 GI:3733006
EST.
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (bases 1 to 673)
REFERENCE
Maizra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. &
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WASHU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; cont
IMAGE Consortium (info@image.llnl.gov) for further infor
MG1:924391
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 467.
FEATURES
Location/Qualifiers
1..673
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/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1
(CACTGTGG) ; Site 2: DralII (CAGCATGTG) ; 1st st:
was primed with an oligo(dT) primer
[ATGTGGCTTTTCTTTTCTTTT]; double-stranded cdi
ligated to a DralII adaptor [TGTGGCCTACTGG], (

```

and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTCTCTTAAAGCTGCG and 3' end primer CGACCTGAGCTCGAGCACA."

as:

Length:	673
Matches:	156
Conservative:	9
Mismatches:	7
Indels:	1
Gaps:	1

-180 (1-222) x A1182368 (1-673)

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UAATCTACTGAGCGGACACCAAGATGAAGGCCACCCCAATGGTTTGTCTTGGTGTC 554
||GlnValIleLysGlyLeuAspIleAlaMetThrAspMetCysProGlyGluLysArg 109
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ysValValIleProProSerPheAlaTyrGlyLysGluGlyTyrAlaGluGlyLysIle 129
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roProAspAlaThrLeuIlePheGluIleGluLeuTyrAlaValThrLysGlyProArg 149
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erileGluThrPheLysGlnIleAspMetAspAsnAspArgGlnLeuSerLysAlaGlu 169
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
GCATTGAACATTTAAGCAATAGACACCGGATTAATGACCGGCAACTCTCCAAAGCTGAG 317
leAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLysProArgAspLysSerTyr 189
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TAGAGCTTTACTTTACAGAGGACTTTGAAAAGATGCAAAACCCCGCTGACAAGTCATAT 257
lnAspAlaValLeuGluAspIlePheLysLysAsnAspHisAspGlyAspGlyPheIle 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
AGNAGGCAGTTTGGAGATATCTTTAAGAAAAATGACCACATGAGGACGGCTTCATT 197
erProLysGluTyrAsnValTyrGlnHisAspGluLeu 222
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d: April 9, 2004, 12:49:58
secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

cleic search, using frame_plus_p2n model

April 9, 2004, 10:40:36 ; Search time 86 Seconds
(without alignments)

1432.548 Million cell updates/sec

US-10-015-480A-180

1189
1 MPKTMHFLRFYFFYLWGL.....HDGDFISPKYNNVYQHDEL 222

BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 1365418

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ameters:

n.model -DEV=xlh

spool/US10015480/runat_07042004_080126_28520/app_query.fasta_1.391

ts NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
S-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humat40.cdi

GN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

FMT=ptco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000

CGN1_1_69 @runat_07042004_080126_28520 -NCPU=6 -ICPU=3

QUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

OP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	971	4	US-09-205-258-33		Sequence 33, Appl
98.9	968	4	US-09-205-258-222		Sequence 222, App
24.9	575	4	US-09-833-381-1564		Sequence 1564, Ap
20.9	570	1	US-07-822-966B-1		Sequence 1, Appl
20.5	562	5	PCT-US92-03993-6		Sequence 6, Appl
20.5	2610	2	US-08-989-386-2		Sequence 2, Appl
16.9	964	4	US-08-023-655-1081		Sequence 1081, Ap
15.7	2157	1	US-08-336-618-25		Sequence 25, Appl
15.6	450	4	US-09-621-976-2544		Sequence 2544, Ap
15.6	675	1	US-08-707-793A-3		Sequence 3, Appl
15.6	675	1	US-08-707-792A-3		Sequence 3, Appl
15.0	571	2	US-08-803-899-1		Sequence 1, Appl

13	176	14.8	2291	4	US-09-220-132-114	Sequenc
14	175	14.7	411	4	US-09-481-620A-84	Sequenc
15	174.5	14.7	327	3	US-09-012-515A-34	Sequenc
16	174.5	14.7	327	3	US-08-360-144A-34	Sequenc
17	174.5	14.7	327	4	US-09-012-504A-34	Sequenc
18	174.5	14.7	327	4	US-09-012-399A-34	Sequenc
19	174.5	14.7	348	3	US-09-012-515A-5	Sequenc
20	174.5	14.7	348	3	US-08-360-144A-5	Sequenc
21	174.5	14.7	348	4	US-09-012-504A-5	Sequenc
22	174.5	14.7	348	4	US-09-012-399A-5	Sequenc
23	174.5	14.7	348	5	PCT-US95-06722-5	Sequenc
24	174.5	14.7	690	4	US-09-481-620A-110	Sequenc
25	174.5	14.7	1137	1	US-08-707-793A-1	Sequenc
26	174.5	14.7	1137	1	US-08-707-792A-1	Sequenc
27	174.5	14.7	1155	1	US-08-707-793A-2	Sequenc
28	174.5	14.7	1155	1	US-08-707-792A-2	Sequenc
29	173	14.6	2246	4	US-09-566-921-48	Sequenc
30	172	14.5	443	4	US-09-833-381-1562	Sequenc
31	167	14.0	2255	2	US-08-741-134-1	Sequenc
32	166.5	14.0	346	4	US-09-621-976-15601	Sequenc
33	166.5	14.0	405	4	US-09-621-976-15602	Sequenc
34	166	14.0	357	4	US-09-328-352-1668	Sequenc
35	165	13.9	459	4	US-09-833-381-693	Sequenc
36	164.5	13.8	879	3	US-08-714-071-3	Sequenc
37	163.5	13.8	672	4	US-09-833-381-697	Sequenc
38	161.5	13.6	269223	4	US-09-596-002-41	Sequenc
39	160	13.5	459	4	US-09-833-381-695	Sequenc
40	155.5	13.1	363	4	US-09-833-381-696	Sequenc
41	152.5	12.8	1236	2	US-08-741-134-5	Sequenc
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43	144	12.1	3591	4	US-09-252-991A-1690	Sequenc
44	136.5	11.5	765	4	US-09-489-039A-3743	Sequenc
45	136	11.4	1401	4	US-09-252-991A-4911	Sequenc

ALIGNMENTS

RESULT 1

US-09-205-258-33

; Sequence 33, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P2007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

:CATION NUMBER: 60/048,882
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 :CATION NUMBER: 60/048,899
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,893
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,900
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,901
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,892
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 :G DATE: 1997-06-06
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 :CATION NUMBER: 60/048,898
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,962
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,963
 :G DATE: 1997-06-06
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 :G DATE: 1997-06-06
 :CATION NUMBER: 60/048,878
 :G DATE: 1997-06-06
 :CATION NUMBER: 60/070,923
 :G DATE: 1997-12-18
 :CATION NUMBER: 60/092,921
 :G DATE: 1998-07-15
 :CATION NUMBER: 60/094,657
 :G DATE: 1998-07-30
 ID NOS: 1227
 entIn Ver. 2.0

mo sapiens

TE

57)

ATION: n equals a,t,g, or c

TE

64)

ATION: n equals a,t,g, or c

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4,448-143 Length:
 1189.00 Matches:

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 4
 Mismatches: 0
 Indels: 0
 Gaps: 0
 US-10-015-480A-180 (1-222) x US-09-205-258-33 (1-971)
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 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGlu
 Db 139 TTTACTGCTCAGAGACAAAGAAAGAGAGAGCACCAGAGAGTGAATAGAA
 QY 41 HisArgProGluLysCysSerLysThrSerLysLysGlyAspLeuLeuAlaIle
 Db 199 CATCGTCCAGAAACCTGCTCTAAGACAAAGAGAGAGAGCTCTAATATGCC
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnSer
 Db 259 GACGGCTACTGCTGCTAAAGAGGCTGGAATTTCTACTGAGCGGACACAAATG
 QY 81 HisProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
 Db 319 CACCCAAATGTTTGTCTTGTGTTGGCAAGTCATAAAGGCTACACATTC
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
 Db 379 ACAGATATGTCCTGAGAAAGAGAGAGAGAGTATATACCCCTTCATTTGCA
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
 Db 439 AAGGAAGGCTATGCAAGAGCAAGATTCACCGGATGCTACATTTGTTGAG
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsp
 Db 499 CTTTATGCTGTGACCAAGGAGGACCGGAGCATTCAGACATTTAAACAAATAGAC
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
 Db 559 AATGACAGGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAGAGGATTT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
 Db 619 GATGAGAAAGCCAGTGCATATCATATCGAGATGCAGTTCATAGAGATATTTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrLysValTyrGln
 Db 679 AATGACCATGATGCTGATGCTTCATTTCTCCCAAGGATACATATGTATACCA
 QY 221 GluLeu 222
 Db 739 GAACATA 744

RESULT 2

US-09-205-258-222
 ; Sequence 222, Application US/09205258
 ; Patent NO. 6525174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: P2007P1
 ; CURRENT APPLICATION NUMBER: US/09/205,258
 ; EARLIER FILING DATE: 1998-12-04
 ; EARLIER FILING DATE: PCT/US98/11422
 ; CURRENT FILING DATE: 1998-06-04
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER FILING DATE: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER FILING DATE: 60/049,375
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER FILING DATE: 60/048,881
 ; EARLIER FILING DATE: 1997-06-06

